GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:52:13 ; Search time 301 Seconds
                                                 (without alignments)
                                                 8895.537 Million cell updates/sec

Title: US-10-643-829-1
Perfect score: 1431
Sequence: 1 ccgtccagaacgtctcaagcg..........ccggtagtaggacggtcctg 1431

Scoring table: IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs. 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents_NA:*
                1: /EMC_Celerra_SID53/ptodata/2/ina/1_COMB.seq:*
                2: /EMC_Celerra_SID53/ptodata/2/ina/5_COMB.seq:*
                3: /EMC_Celerra_SID53/ptodata/2/ina/5A_COMB.seq:*
                4: /EMC_Celerra_SID53/ptodata/2/ina/6A_COMB.seq:*
                5: /EMC_Celerra_SID53/ptodata/2/ina/6B_COMB.seq:*
                6: /EMC_Celerra_SID53/ptodata/2/ina/7_COMB.seq:*
                7: /EMC_Celerra_SID53/ptodata/2/ina/H_COMB.seq:*
                8: /EMC_Celerra_SID53/ptodata/2/ina/PCTUS_COMB.seq:*
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               10: /EMC_Celerra_SID53/ptodata/2/ina/RE_COMB.seq:*
               10: /EMC_Celerra_SID53/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1431	100.0	44378	3	US-09-949-016-12540	Sequence 12540, A
2	909.4	63.5	1237	3	US-09-007-678B-48	Sequence 48, Appl
3	703.6	49.2	84875	3	US-09-949-016-17334	Sequence 17334, A
4	703.6	49.2	84875	3	US-09-949-016-17335	Sequence 17335, A
5	703.6	49.2	84875	3	US-09-949-016-17336	Sequence 17336, A
6	703.6	49.2	84875	3	US-09-949-016-17337	Sequence 17337, A
7	703.6	49.2	85152	3	US-09-949-016-12665	Sequence 12665, A
8	703.6	49.2	85152	3	US-09-949-016-12666	Sequence 12666, A
9	703.6	49.2	85152	3	US-09-949-016-12667	Sequence 12667, A
10	703.6	49.2	85152	3	US-09-949-016-12668	Sequence 12668, A
11	701	49.0	3798	3	US-09-023-655-887	Sequence 887, App
12	281.2	19.7	512	3	US-09-949-016-4540	Sequence 4540, Ap
13	279.5	19.5	512	4	US-09-880-107-2282	Sequence 2282, Ap
14	279.4	19.5	9153	3	US-09-949-016-15183	Sequence 15183, A
15	249.2	17.4	187595	3	US-09-949-016-15546	Sequence 15546, A
16	247.8	17.3	422	3	US-09-397-787-186	Sequence 186, App
17	220.6	15.4	3227	3	US-09-976-594-775	Sequence 775, App
18	203.4	14.2	237	3	US-09-397-787-89	Sequence 89, Appl
19	189.4	13.2	211049	3	US-09-949-016-15770	Sequence 15770, A
20	180.6	12.6	309	3	US-09-313-294A-7018	Sequence 7018, Ap
21	177	12.4	6727	3	US-09-949-016-16282	Sequence 16282, A
22	163.4	11.4	464	3	US-09-774-528-63	Sequence 63, Appl
23	163.4	11.4	464	3	US-10-120-988-63	Sequence 63, Appl
24	146.4	10.2	2124	10	5428012-1	Patent No. 5428012
25	146.4	10.2	2124	10	5451506-1	Patent No. 5451506
26	143.6	10.0	103377	3	US-09-949-016-14089	Sequence 14089, A
27	142.2	9.9	90541	3	US-10-759-359A-3	Sequence 3, Appli
28	142.2	9.9	90541	3	US-10-207-973-3	Sequence 3, Appli
29	142.2	9.9	156651	5	US-10-799-676-3	Sequence 3, Appli
30	142.2	9.9	156651	3	US-09-949-016-17349	Sequence 17349, A
31	140.4	9.8	376	3	US-09-949-016-3441	Sequence 3441, Ap
32	114	8.0	1534	2	US-08-480-784-13	Sequence 13, Appl
33	114	8.0	1534	2	US-08-483-553-13	Sequence 13, Appl
34	114	8.0	1534	2	US-08-487-002-13	Sequence 13, Appl
35	114	8.0	1534	2	US-08-483-554B-13	Sequence 13, Appl
36	114	8.0	1534	2	US-08-488-011B-13	Sequence 13, Appl
37	114	8.0	1534	2	US-08-850-727-13	Sequence 13, Appl
38	114	8.0	1534	7	PCT-US95-10202-13	Sequence 13, Appl
39	114	8.0	1534	7	PCT-US95-10220-13	Sequence 13, Appl
40	114	8.0	1534	7	PCT-US95-10203-13	Sequence 13, Appl
41	114	8.0	1924	2	US-08-480-784-14	Sequence 14, Appl
42	114	8.0	1924	2	US-08-483-553-14	Sequence 14, Appl
43	114	8.0	1924	2	US-08-487-002-14	Sequence 14, Appl
44	114	8.0	1924	2	US-08-483-554B-14	Sequence 14, Appl
45	114	8.0	1924	2	US-08-488-011B-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-12540
Sequence 12540, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 12540
;   LENGTH: 44378
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(44378)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12540

  Query Match   100.0%; Score 1431; DB 3; Length 44378;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCGTCCAGAACGTCTCAGGAGAGCTCACGACGGCGAGTCACGTTTTTTCCCCCCCTCTAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 CCGTCCAGAACGTCTCAGGAGAGCTCACGACGGCGAGTCACGTTTTTTCCCCCCCTCTAC 663

Qy   61 ATTGCAGATGTGGCTCCCAAATGTTGACGTTGGCCAGGACCTTTGCAAACAAGCCAGGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664 ATTGCAGATGTGGCTCCCAAATGTTGACGTTGGCCAGGACCTTTGCAAACAAGCCAGGCCA 723

Qy   121 AAAAGTTTCAAATATTTACACTGGCTGCTTTAATAAGGGCATTGATCTTATCCTCCGTAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   724 AAAAGTTTCAAATATTTACACTGGCTGCTTTAATAAGGGCATTGATCTTATCCTCCGTAAA 783

Qy   181 GGTCACCTCATAGTCCTGCAGAATGAGGGCAGATAGATGCCAGGCAAGCTGGGGAGGACGGA 240

RESULT 2
US-09-007-678B-48

; Sequence 48, Application US/09076788
; Patent No. 6342483
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: OBERMILLER, PATRICE S.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER
; FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2
; CURRENT APPLICATION NUMBER: US/09/007,678B
; CURRENT FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 08/373,799
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 08/182,961
; PRIOR FILING DATE: 1994-01-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: MicroSoft WordPad
; SEQ ID NO 48
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-007-678B-48

Query Match 63.5%; Score 909.4; DB 3; Length 1237;
Best Local Similarity 94.0%; Pred. No. 6.6e-277;
Matches 999; Conservative 0; Mismatches 36; Indels 28; Gaps 4;

Qy   381 CACAGTTTAATTTATTCTGTAATTCCCACGCTTTACTGTTGCCACGGAA---------- 429
           ||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   131 CGCAGTTTTAATTTATTCTGTAATTCCCGTTGCCACGGAAACCAAGGGGGCT 190

Qy   430 ACCGGCTGAGCAATAGCCTCTCAGAATAGGAAAATCAAGACACACTCAGAGAGGGGGGA 489
Db   191 ACCCCTAGCACAGCAGCCCTCAGAATACCAAAATCAGAGAGGAAGGGGAGGGA 250

Qy   490 CAGAGAAAAGAGCCTAGCATCTCTCGGGGGTTGGGCCACCCCAGTCCTCCCCTGG-TGA 548
Db   251 CAGAAAAGAGCCAAGCGTCTCTCGGGANTGGGCCACCCAGTCTCGCCCCGGATGA 310

Qy   549 CATAAAAAGAAAAGAGAGAGGAAGAAATTCACCTGAGTTCGCGTAAAAGGCCCCGC 608
Db   311 CGTAAAAAGGAAAAGAGAGAGGAAGAAATTCACCTGAGTTCGCGTAAAAGGCCCCGC 370

Qy   609 CCTCTCGCCTCTACGCTTCCAGTTGCGCGTTATTACGTCACAGTAATTGCTG 668
Db   371 CCTCTCGCCTCTACGCTTCCAGTTGCGCGTTATTACGTCACAGTAATTGCTG 430

Qy   669 TCAGAATGGCCCACCTGAGGCCTAAGATAGTGTCCAAAGCAGTCTTAAG 728
Db   431 TCAGAATGGCCCACCTGAGGCCTAAGATAGTGTCCAAAGCAGTCTTAAG 490

Qy   729 AAGAGGTCCCATTACCCCACTCTTTCCCGCCCTAATGGAGGAGTCTCCAGTTTAGGTAAATAA 788
Db   491 AAGAGGTCCCATTACCCCACTCTTTCCCGCCCTAATGGAGGAGTCTCCAGTTTAGGTAAATAA 550

Qy   789 AAGGAATTGTTGGGAGGTGGAGGGGAAAAGAACTACTATTTCCAACATGCATTGCGGAACGAA 848
Db   551 AAGGAATTGTTGGGAGGTGGAGGGGAAAAGAACTACTATTTCCAACATGCATTGCGGAACGAA 610

(sequence alignment continues)

RESULT 3
US-09-949-016-17334/c
; Sequence 17334, Application US/09949016
; Patent No. 681233⁹
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 17334
;   LENGTH: 84875
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17334

  Query Match   49.2%; Score 703.6; DB 3; Length 84875;
  Best Local Similarity   85.0%; Pred. No. 1e-210;
  Matches 910; Conservative   0; Mismatches 105; Indels 51; Gaps   9;

Qy   381 CACAGTTTTAATTATCTGTAATTCCCACGCTTTACTGTTGGCCACGGAA--------------------------- 429

RESULT 4
US-09-949-016-17335/c

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; Sequence 17335, Application US/0994901b
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 17335
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 84875
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17335

Query Match             49.2%;  Score 703.6; DB 3;  Length 84875;
Best Local Similarity   85.0%;  Pred. No. 1e-210;
Matches 910; Conservative  0; Mismatches 109; Indels  51; Gaps  9;
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Qy    381 CACAGTTTTAATTTATTCTGTAATTCCCACGGCTTTTACTGTTGCCACGGAA------------ 429
          ||||||||||||||||||||| ||||||||||||||| || |||||||||||
Db   1732 CGCAGTTTTAATTTATTCTGTAATTCCCGGTTTGCCACGGAAAAACCAAGGGGCT 1673

Qy    430 ACCGCTGAGCAATAGCCTCTCAGAATATAGGAAAATCAAGACACAGTCAGAGGGCGCGGGA 489
          ||||  ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   1672 ACCGCTAAGCAGCAGCCCTCTCAGAATACCGAAATCAAGGTACAATCAGAGGATGGGAGGA 1613

Qy    490 CAGAAAGAGAGCCTAGCACATCTCTCGGGGGTTGGGCCACCCAGTCCTTCCCCCTGG-TGA 548
          |||||||||||||||||| ||||||||||| ||||||||||||||||||||||||| |||
Db   1612 CAGAAAGAGCCAAGCGTCTTCTCGGGATTGGGCCACCCAGTCTGCCCCCGGATGA 1553

Qy    549 CATAAAAAGAAAGGAGACGGAAAAAAGGAAGAAATTCTACCTGAGTTCGCCGTAAAGCCCCGC 608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1552 CGTAAAAGGAAAGAGAGGAGAAGGAAGAATTCTACCTGAGTTTGCCATAAAAGTGCCTGC 1493

Qy    609 CCTCTCGCCTCTACGGCTTCCCAGTTGCGCGGCTTATTACGTCACAGTAATTGCTGTACCAAGG 668
          |||||||||||||||||||||||||||||| ||||||||||||||||
Db   1492 CCTCTCAGCCTCTACTCTTCCAGTTGCGCGGCTTATTGCATCACAGTAATTGCTGTACGAAGG 1433

Qy    669 TCAGAAATCGGCCACACCTGAGGCCTGAAGATAGTAGTGTGCCAAAGCAGTCTTTAAG 728
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1492 CCTCTCAGCCTCTACTCTTCCAGTTGCGCGGCTTATTGCATCACAGTAATTGCTGTACGAAGG 1433

Qy    729 AAGAGGTCCATTACCCCACTCTTTCCGCCCTAATGAGGAGGTCTCCAGTTAGGTAAATAA 788
          ||||||||||||||||||||  ||||||| |||||
Db   1432 TCAGAAATCGGCTACC-------------------TATTGTCCAAAGCAGTCGTTAAG 1397

Qy    789 AAGGATTGTTGGGAGGTGGGGGAAAG----AACTACTATTTCCAACATGCATTGCCGA 843
          |||||||||| ||||||||||||||||     |||||||||| |||||||||||||||
Db   1396 AAGAGGTCCAATCCCCCACTCTTTCCGCCCTAATGGAGGTCTCCAGTTTCGGTAAATAT 1337

Qy    844 ACGAAAAGGCCCTTCGGCCCACACTGTTCCTTGGAAAACTGTAGTCTTGATGGAGGAACATCCA 903
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 ATGAAAAGGTCTTCGCCACAGTGTTCCTTAGAAACTGTAGTCTTTATGGAGGAGAACATCA 1217

Qy    904 ATACCAAAGCGGGGCACAATTCTCACGGGAAATCCAGTGGGATAGATTGGGAGACCTCCGCGGG 963
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 ATGAAAAGGTCTTCGCCACAGTGTTCCTTAGAAACTGTAGTCTTTATGGAGGAGAACATCA 1217

Qy   1024 AGACTAGGCCAAAAAAAGATACCTACACAACTC-CTAGGAAGACTACACGATTCCCATCCAGCC 1082
          ||||||||||||||||||||||
Db   1156 CTTGTACTTGTCAACAGTTATGGACTGGAG---TGTTATGTTTTCGTATTTTGAAAGCAG 1100

Qy    964 CTTATACATGTCAAACAGTAATGGAATTGGAGTTGTTGTTGTTTCTTCCCTATCTTGAGAGCAG 1023
          | |  |||||||||||||||||||||||||||||||||||||| |||||||
Db   1156 CTTGTACTTGTCAACAGTTATGGACTGGAG---TGTTATGTTTTCGTATTTTGAAAGCAG 1100

Qy   1216 ATACCAGAGCGCGGGCACAATTCTCACGGAAATCCAGTGGATAGATTGGGAGACCTGTGCCGC 1157
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1276 ATGAAAAGGTCTTCGCCACAGTGTTCCTTAGAAACTGTAGTCTTTATGGAGGAGAACATCA 1217
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RESULT 5
US-09-949-016-17336//c
; Sequence 17336, Application US/0994901b
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17336
; LENGTH: 84875
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17336

Query Match             49.2%;  Score 703.6; DB 3;  Length 84875;
Best Local Similarity   85.0%;  Pred. No. 1e-210;
Matches 910; Conservative  0; Mismatches 109; Indels  51; Gaps  9;
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Db   1099 AAACTAGGCCTTAAAAAGATACGTACAAACTCTTTAGGGAGGACTACAAATTCCCATCCAGCC 1040

Qy   1083 CCACGAGTCTCCGGCGAAGTAGTCCCTCTAAGGTCACAGTGGGCCTTGCGGGGGGACGGCAGTGGGCGC 1142

Db   1039 CCAGGAGTCTGGGGCGAGTAGTCCTGTAAGGTCATAGTGGCCTTGCGGGGGGACGGCAGTGACGC 980

Qy   1143 CGAATTTGCCTGGGGAAGGGGGAAAATCCGGCTCTGGGCCCACAATCTGCGCACTCCTAGTTCG 1202

Db    979 CGAATTTGCCTGGGGGCGAGGGGGGAAATGCGCTTCTGGGCCCCATGTCTTGCGGCCACTCGTAGTTCCA 920

Qy   1203 CCCCTTCAGCCTCAATGTTTGTTATTGTTGTTTCGGGGTTTCAGGTTGCTTCGTTGCCCGCCG-CCCC 1261

Db    919 CCCCTTCAGCCCCCAGTTGTTTGTTA----TTTTTCGGGGTTCAGCTTGCTTTTGCCCGGTCTCC 863

Qy   1262 ATCGACGGCAAATCTCCACCAATCAATGGGGTCGGTCGTTTGGAGGGACAAGGTGGTGAGAGCC 1321

Db    862 GTCGACGCAAATCGCCACCAGTCAATGGGGTGGTCGTTTTGAGGGACAAGGTGGTAAGAGCC 803

Qy   1322 AATCATCTTGGCGAACACTCGGGAGAAAACAGGGAGGACTAGTTAGTCTGTCTTTAATCCGCCAATGT 1381

Db    802 AATCTTCTTGGCGAAAACGGGAGAAAC--GGGACTAGTTACTGTCTTTGGTTCGCGCCCATGT 745

Qy   1382 TAGATTCACCCCACAGGGGATTAGCGCGGCCAGAGCCCGGTTAGCGGCGACCGGGTGCCTTG 1431

Db    744 TAGATTCACCCCACACAGATTAGCGCGCAGAGCTGGCAGCGCGACCGGTCTTTG 695
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Qy    381 CACAGTTTTAATTTATTCTGTAATTCCCACGGCTTTTACTGTTGCCACGGAA------------ 429
          |||||||||||||||||| || ||||||||||||||| || |||||||||||
Db   1732 CGCAGTTTTAATTTATTCTGTAATTCCCGGTTTGCCACGGAAAAACCAAGGGGCT 1673

Qy    430 ACCGCTGAGCAATAGCCTCTCAGAATATAGGAAAATCAAGACACAGTCAGAGGGCGCGGGA 489
          ||||  |||||||||||||||||||||||||||||||||||||||||||
Db   1672 ACCGCTAAGCAGCAGCCCTCTCAGAATACCGAAATCAAGGTACAATCAGAGGATGGGAGGA 1613

Qy    490 CAGAAAGAGAGCCTAGCACATCTCTCGGGGGTTGGGCCACCCAGTCCTTCCCCCTGG-TGA 548
          ||||||||||||||||||||||||||| |||||||||||||||||||||||| |||
Db   1612 CAGAAAGAGCCAAGCGTCTTCTCGGGATTGGGCCACCCAGTCTGCCCCCGGATGA 1553

Qy    549 CATAAAAAGAAAGGAGACGGAAAAAAGGAAGAAATTCTACCTGAGTTCGCCGTAAAGCCCCGC 608
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   1552 CGTAAAAGGAAAGAGAGGAGAAGGAAGAATTCTACCTGAGTTTGCCATAAAAGTGCCTGC 1493

Qy    609 CCTCTCGCCTCTACGGCTTCCCAGTTGCGCGGCTTATTACGTCACAGTAATTGCTGTACCAAGG 668
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Db    668
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RESULT 6
US-09-949-016-17337/c
; Sequence 17337, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17337
; LENGTH: 84875
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17337

Query Match   49.2%;   Score 703.6; DB 3; Length 84875;
Best Local Similarity   85.0%;   Pred. No. 1e-210;
Matches 910; Conservative   0; Mismatches 109; Indels 51; Gaps 9;

Qy   1492 CCTCTAGCCTCTACTCTTTCCGAGTTGCGGCTTATTGCATCACAGTAATTGCGTACGAAGG 1433
Db   CACAGTTTAATTTATCTGTAATTCCCACGCTTTACTTTACTGTTGCCACGGAA 1732

Qy   669 TCAGAATCGCCACCTGAATATCAGGTAAGCAGTAGTGTCCAAAGCAGTCTTAAG 728
Db   1672 ACCGCTAAGCACGCAGCCTTCTCAGAATACGAAATCAACAGTCAGAGGAGGGCGGGA 1673

Qy   1432 TCAGAATCGCTACC---------TATTGTCCAAAAGCAGTCGTAAG 1397
Db   430 ACCGCTGAGCAAATAGCCTCTCAGAATAGGAAATCAACAGTCAGAGGAGGGCGGGA 489

Qy   729 AAGAGGTCCCATTACCCCACTCTTTCCGCGTTCCAGTTTAGGTAAATAA 788
Db   1672 ACCGCTAAGCACGCAGCCTTCTCAGAATACGAAATCAACAGTCAGAGGAGGGCGGGA 1613

Qy   1396 AAGAGGTCCCAATCCCCCACTCTTTCCGCCCGTTAAATGGAGGTCCCAGTTTCCGTAAATAT 1337
Db   490 CAGAAGAGAGCCTAGCAATCTTCGGGGGTTGGGCACCCAGTCCTTCCCCTTGG-TGA 548

Qy   789 AAGGATTGTTGGGAGGTGGGACGGGAAAG------AACTACTATTTCCAACATCCATTGCGGA 843
Db   1612 CAGAAAGAGACCAAAGCGTGCTTCGGGGGTGGGACGGGGATGA 1553

Qy   1336 AAGTAATAAAGGATTGTTGGGGGGTGCAGGGAAAATAATTATTTCCAGCATCCGTTCGGA 1277
Db   549 CATAAAAAAGAAGAGACAGGGAAAAAGGAAGAAATTCTACCTGAGTTGCCATAAAGTGCCTGC 608

Qy   844 ACGAAAAGGCCTTGGGCCACACTGTTCCTTGGAAACTGAGTCTTATGGAGAGGAACATCCA 903
Db   1552 CGTAAAAGGAAGAGGACGGGAAAGGAAGAAATTCTACCTGAGTTGCCATAAAGTGCCTGC 1493

Qy   1276 ATGAAAGGTCTTCGCCACAGTTGTTCCTTAGAAACTGAGTCTTATGGAGAGGAACATCCA 1217
Db   609 CCTCTCAGCCTCTACTCTTCCAGTTGGGGTTTATTACGTCACAGTTAATTGCTGTACGAAGG 668

Qy   904 ATACCAAAAGGGGGCACAAATTCTTCACGGAAAATCCAGTGGAGTAGAATTGGGAGAACCTCCGCGGGG 963
Db   1492 CCTCTAGCCTCTACTCTTCCAGTTGCGGCTTATTGCATCACAGTTAATTGCTGTACGAAGG 1433

Qy   1216 ATACCAGAGAGCGGGGCGCAAATTCTCACGGAAAATCCAGTGGGGATAGAATCGTGTGGCG 1157
Db   669 TCAGAATCGCCACCTGAGGGCCTGAAATATCAGGTAAGCAGTAGTGTCCAAAGCAGTCTTAAG 728

Qy   964 CTTATACATGTCAACAGTAATGGATTGGGAGTGTTGTTAATGTTCTCCCTATCTTGAGACGAG 1023
Db   1432 TCAGAATCGCTACC-----TATTGTCCAAAAGCAGTCGTAAG 1397

Qy   1156 CTTGTACTTGTCAACAGTTATGGACTGGGAG---TGTTATGTTTCGTATTTGAAAGCAG 1100
Db   729 AAGAGGTCCCATTACCCCACTCTTTCCGCGTTCCAGTTTAGGTAAATAA 788

Qy   1024 AGACTAGGCCAAAAAAGGATTACCTACAAACTC--CTAGGAAGAGACTACGATTCCCATCCAGCC 1082
Db   1432 TCAGAATCGCTACC 1397

Qy   1099 AAACTAGGCCTTAAAAAGGATTACGTACAACTCTTTAGGGAGGACTACAAATTCCCATCCAGCC 1040
Db   549 CATAAAAAGAAGAGACAGGGAAAAAGGAAGAAATTCTACCTGAGTTGCCATAAAGTGCCTGC 608

Qy   1083 CCACGGAGTCTCGGGGCAAGTAGTCAGTGTGGTCGCCTGCGGGGGGGACGGCAAGTGGGCGC 1142
Db   1612 CAGAAAGAGACCAAAGCGTGCTTCGGGGGTGGGACGGGGATGA 1553

Qy   1262 ATCGACGCAAATCTCCACCAATCAATCAAATGGGCGTGGTCGTTTGAGGGGACAAGTGGTGAGAGCC 1321
Db   862 GTCGACGCAATCGGCCACCAGTCAATGGGGTGGTCGTTTTGAGGGACAAGTGGGTAAGAGCC 803

Qy   919 CCCCTCAGCCCCCAGTGTTTGTTA---TTTTTCGGGTTCAGCTTGCTTTGCCCCGTCTCC 863
Db   1203 CCCCTCAGCCTCAAATGTTTTGCTTATTGTTCTTCGGCTTCTGCCCCCG-CCCC 1261

Qy   1203 CGAATTTGCCTGGGGGCCAGGGGGGAAAATGGCGCTCTGGGCCCATGTCAGTTCCA 1202
Db   979 CGAATTTGCCTGGGGGCCAGGGGGGAAAATGGCGCTAGTTCCA 920

Qy   1143 CGAATTTGCCTGGGGAAGGGGGAAATCCGCTCTGGGCCCACATCCTCTAGTTCCG 1202
Db   979 CGAATTTGCCTGGGGGCCAGGGGGGAAAATGGCGCTAGTTCCA 920

Qy   1039 CCAGGAGTCTGGGGCAAGTAGTCCTGTAAGGTCAGTGGCCGTTGAGGAACGCGAGTGAGCGC 1038
Db   1083 CCACGGAGTCTCGGGGCAAGTAGTCAGTGTGGTCGCCTGCGGGGGGGACGGCAAGTGGGCGC 1142

Qy   1083 CCACGGAGTCTCGGGGCAAGTAGTGAGTAGTCGCCTGCGGGGGGGACGGCAAGTGGGCGC 1142

Qy   1099 AAACTAGGCCTTAAAAAGATTACGTACAACTCTTTAGGGAGGACTACAAATTCCCATCCAGCC 1040
Db   1024 AGACTAGGCCAAAAAAAGATTACCTACAAACTC--CTAGGAAGAGACTACGATTCCCATCCAGCC 1082

Qy   1024 AGACTAGGCCAAAAAAGGATTACCTACAAACTC--CTAGGAAGAGACTACGATTCCCATCCAGCC 1082

Qy   549 CATAAAAAAGAAGAGACGGGGAAAAAGGAAGAAATTCTACCTGAGTTGCCATAAAGTGCCTGC 608

Qy   490 CAGAAGAGAGCCTAGCAATCTTCGGGGGTTGGGCACCCAGTCCTTCCCCTTGG-TGA 548

Qy   1612 CAGAAAGAGACCAAAGCGTGCTTCTCGGGATTGGCCACCCAGTCTTGCCCCGGATGA 1553

Qy   669 TCAGAATCGCCACCTGAAATATCAGGTAAGCAGTAGTGTCCAAAGCAGTCTTAAG 728

Qy   1432 TCAGAATCGCTACC 1397

Qy   789 AAGGATTGTTGGGAGGTGGGACGGGAAAG------AACTACTATTTCCAACATCCATTGCGGA 843

Qy   1336 AAGTAATAAAGGATTGTTGGGGGGTGCAGGGAAAATAATTATTTCCAGCATCCGTTCGGA 1277

Qy   844 ACGAAAAGGCCTTGGGCCACACTGTTCCTTGGAAACTGAGTCTTATGGAGAGGAACATCCA 903

Qy   904 ATACCAAAAGGGGGCACAAATTCTTCACGGAAAATCCAGTGGATAGATTGGGAGAACCTCCGCGGGG 963

Qy   1276 ATGAAAGGTCTTCGCCACAGTTGTTCCTTAGAAACTGAGTCTTATGGAGAGGAACATCCA 1217

Qy   1216 ATACCAGAGAGCGGGGCGCAAATTCTCACGGAAAATCCAGTGGGGATAGAATCGTGTGGCG 1157

Qy   964 CTTATACATGTCAACAGTAATGGATTGGGAGTGTTGTTAATGTTCTCCCTATCTTGAGACGAG 1023

Qy   1156 CTTGTACTTGTCAACAGTTATGGACTGGGAG---TGTTATGTTTCGTATTTGAAAGCAG 1100

Qy   1262 ATCGACGCAATCTCCACCAATCAATCAAATGGGCGTGGTCGTTTGAGGGGACAAGTGGTGAGAGCC 1321

RESULT 7

Db 862 GTCGACGGAATCGCCACCAGTCAATGGGGTGGTGGTCGTTTTTGAGGGACAAAGTGGTAAGAGCC 803
          ||||||| ||||||||||||||||||||||||||| || |||||||| ||||||||||||||||
Qy 1322 AATCATCTTGGCGACACTCGGAGAAACAGGGAGACTAGTTACTGTTCTTATCCGGCCATGT 1381

Db 802 AATCTTCTTGGCGAAAAACGCCGAGAAAC--GGGACTAGTTACTGTCTTTGTCCGCCATGT 745
          |||| |||||||| |||| ||| ||||||| ||||||||||||||| | ||||||||||||
Qy 1382 TAGATTCACCCCACAGGGGATAGCGCGGAGAGCCGGTAGCGGAGCGGGTCCTTG 1431

Db 744 TAGATTCACCCCACAGAGGATAGCGCGCAGAGCTGGCAGCGGGACGGGTCCTTTG 695

; Sequence 12665, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12665
; LENGTH: 85152
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12665

RESULT 7
US-09-949-016-12665/c

Query Match   49.2%; Score 703.6; DB 3; Length 85152;
Best Local Similarity 85.0%; Pred. No. 1e-210;
Matches   910; Conservative   0; Mismatches 109; Indels 51; Gaps   9;

Qy 381 CACAGTTTTAATTTATCTGTAATTCCCACGCTTTACTGTTGTTCCACGGAA----------- 429
          |||||||| ||||||| |||||||||||| ||| |||||||||| |||||||
Db 2009 CGCAGTTTAATTTATTCTGTAATTCCCGTTGCCACGGAAAACCAAGGGGCT 1950

Qy 430 ACCGCTGAGCAAATAGCCTCTCAGAATAGAGAAATCAAAGACACAGTCAGAGAGAGGCGGGGA 489
          |||||| || || |||||||||||| |||| |||||| |||||||||||||||||||||||
Db 1949 ACCGGTCAGAATACGAAATCAAGGTTACAATCAGAGGATGGGAGGGA 1890

Qy 490 CAGAAAGAGCCTAGCATCTTCGGGGCGTTGGGCCACCCAGTCTCTCCCTGG-TGA 548
          |||||| || ||||||||||||||||||||||||||| ||||||||| |||||
Db 1889 CAGAAGAGCCAAGCGTCTTCTCGGGGCTTCTGGATTGGCCACCCAGTCTTGCCCCCGGATGA 1830

Qy 549 CATAAAAAGAGAGACGGAAAAAGGAAGAGAATTCTACCTGAGTTGTTCGGCCGCGCCGC 608
          ||||| ||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db 1829 CGTAAAAGGAAAGAGAACGGAAGAAGAAATTCTACCTGAGTTTGGCCATAAAAGTGCCTGC 1770

Qy 609 CCTCTCGCCTCTCACGCTTCCAGTTGCCGGCTTATTACGTCACAGTAATTGCTGTACCAAGG 668
          |||||||||||||||||||||||||||||||||||| |||||||| ||||| |||||||||
Db 1769 CCCTAGCCTCTACTCTTCCAGTTGCGGCTTATTGCATCACAGTAATTGCTGTACGAAGG 1710

Qy 669 TCAGAATGGCCACCTGAGGCCTGAAATATCAGCGGTAAGATAGTGTCCAAAGCAGTCTTAG 728
          |||||||||||||||||||||| |||||||||||||| ||| || |||||||||||||| |
Db 1889 CAGAAGAGCCAAGCGTCTTCTCGGGGCTTCTGGATTGGCCACCCAGTCTTGCCCCCGGATGA 1830

Qy 729 AAGAGGTCCCATTACCCCACTCTCTTTCCCGCCCTAATGATGGAGGTCTCCAGTTTAGGTAAATA 788
          |||| |||||||| ||||||| |||||| ||||| |||| |||||||||||| || |||||||
Db 1673 AAGAGGTCCAATCCCCCACTCTTTCCCGCCCTAATGGAGGTCTTCCAGTTTCGGTAAATAT 1614

Qy 669 TCAGAATGGCCACCTGAGGCCTGAAATATCAGCGGTAAGATAGTGTCCAAAGCAGTCTTAG 728
          |||||||||||||||||||||| |||||||||||||| ||| || |||||||||||||| |
Db 1769 CCCTAGCCTCTACTCTTCCAGTTGCGGCTTATTGCATCACAGTAATTGCTGTACGAAGG 1710

Qy 1709 TCAGAATCGGCTACC------------ 1674
          |||||||| ||| |
Db 1709 ----------TATTGTCCAAAGCAGTCGTAAG 1674

Qy 789 AAGGATTGTTGGGAGGTGGAGGGAAAG-----AACTACTATTTCCACACATGCATTGCGGA 843
          |||| ||| ||||| |||||||||||| |||| ||||||| |||||| |||||||||
Db 1613 AAGTAATAAGGATTGTTCGGGAGGGTGGGGGTGGGGGGGAAATAATTAATTATTTCCAGCACATGCCGTTGCGGA 1554

RESULT 8

Qy 844 ACGAAAGGCCTTGGCCACACTGTTCCTTGGAAACTGTAGTCTTTATGGAGGAGGAACATCCA 903
          |||||| ||| ||||||||| |||||||| |||||||||||||||||||||||||||||||
Db 1553 ATGAAAAGGTCTTCGCCACAGTGTTCCTTAGAAACTGTAGTCTTTATGGAGGAGGAACATCCA 1494

Qy 904 ATACCAAAAGCGGGGCACAAATTCTCACGGAAAATCCAGTGGATAGATTGGAGACTTGCGGG 963
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1493 ATACCAGAGCGGGGCACAAATTCTCACGGAAAATCCAGTGGATAGATTGGAGACTTGCGGG 1434

Qy 964 CTTATACATGTCAACACAGTAATGGATTGGAGGTTGTTGTTATGGTTCTCCTATCTTGAGAGCAG 1023
          ||| ||| |||||||||||| ||||||||||| |||||| ||||| |||||||||||||||
Db 1433 CTTGTACTTGTCAACACAGTTATGGACTGGAG---TGTTATGTTTTTTCGTATTTTGAAAGCAG 1377

; Sequence 12666, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12666
; LENGTH: 85152
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12666

RESULT 8
US-09-949-016-12666/c

Query Match   49.2%; Score 703.6; DB 3; Length 85152;
Best Local Similarity 85.0%; Pred. No. 1e-210;
Matches   910; Conservative   0; Mismatches 109; Indels 51; Gaps   9;

Qy 1024 AGACTAGGCCAAAAAAAGATAACCTACACACTC-CTAGGAAGAGACTAGCGATTCCCATCCAGCC 1082
          ||||| ||||||||||| |||| || |||||||| ||||| ||| ||||||||||||||||||
Db 1376 AAACTAGGCCTTAAAAAGATACGTACAAACTCTTTAGGGAGGAGACTACAAATTCCCATCCAGCC 1317

Qy 1083 CCACGAGTCTCGGGGCAAAGTAGTCTCCTTAAGGTCACAGTGGCCTCTGAGGGGACGGAGTGGGCGC 1142
          || || || ||||||||| |||| || ||||||| ||| |||| |||| ||||||||||||||||
Db 1316 CCAGGAGTCTGGGGCAAGTAGTCCTGTGTAAGGTCAGTGTGGGCGGGGCGGGGGACGGAGTGAGCGC 1257

Qy 1143 CGAATTTGCCTCGGGGAAGGGGAAAATCGGCTCTGGCCCACACATCTGCGGCACTCCTAGTTCCG 1202
          |||||||||||||||||| |||||| |||||| ||||||||||| ||| || |||||||||||||
Db 1256 CGAATTTGCCTGGGGCGGGAGAAAATCCGCTCTGGGCCCCATGTCTCGCGGGCACTCGTAGTTCCA 1197

Qy 1203 CCCCTCAGCCTCAATGTTGTGTATTCGTTGTGGGGTTCAGGTTGCTTCTGCCCCG--CCCC 1261
          ||||||||| |||||| ||| |||| || ||||||||||||| || |||| |||| ||||
Db 1196 CCCCTCAGCCCCAGTGTTTGTTA---TTTTTCGGGTTCAGCTGCTTGCTTTTGCCCCGTCTCC 1140

Qy 1262 ATCGACGCAATCTCCACCAATCAATCATGGGGTGGTGGTGGTCGTTTCTTTTGAGGGCAAGAGCC 1321
          ||||| |||||| ||||||||| || |||| | ||||||||||||||| ||||||||| |||||
Db 1139 GTCGACGGAATCGCCACCAGTCAATGGGGTGGTGGTGGTCGTTTCTTTTGAGGGCAAGTGGTAAGAGCC 1080

Qy 1322 AATCATCTTGGCGACACTCGGAGAAACAGGGAGGACTAGTTACTGTTCTTATCCGGCCATGT 1381
          |||| ||||||| ||||||||||||||||||||| |||||||||||||| |||||||||||||
Db 1381 ----GGGACTAGTTACTGTCTTTTGTCCGCCATGT 1022

Qy 1382 TAGATTCACCCCACAGAGGATAGCGCGGAGAGCCGGTAGCGGAGCGGGTCCTTG 1431
          |||||||||||||| |||||||||| |||||||||||||||||||||||||||
Db 1021 TAGATTCACCCCACAGAGGATAGCGCGCAGAGCTGGCAGCGGGACGGGTCTTG 972

Qy 381 CACAGTTTTAATTTATCTGTAATTCCCACGCTTTACTGTTGTTCCACGGAA----------- 429
          |||||||| ||||||| |||||||||||| ||| |||||||||| |||||||
Db 2009 CGCAGTTTAATTTATTCTGTAATTCCCGTTGCCACGGAAAACCAAGGGGCT 1950

RESULT 9
US-09-949-016-12667/c
; Sequence 12667, Application US/0949016

Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12667
; LENGTH: 85152
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12667

Query Match 49.2%; Score 703.6; DB 3; Length 85152;
Best Local Similarity 85.0%;   Pred. No. 1e-210;
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

```
Qy   1083 CCACGGAGTCTCGGGCCAAGTAGTAGTCTTCTCTTAAGGTTCAGTGGGCTTGCGGGGGCG 1142
          ||||||| |||||||||||||||| ||||||||| |||||||||||||||||||||||||
Db   1769 CCTCTAGCCTTCTACTCTTCCAGTTGCGGGCTTATTGGCATCACAGTAATTGCTACGGAAGG 1710

Qy   1316 CCAGGAGTCTGGGGGCAAGTAGTCCTTGTAAGGTCAGTGGCCTCGCGGGGGACGGCAGCGC 1257
          |||||||
Db    669 TCAGAATCGCCACCTGAGGCGTCGAATATCAGCGTAAGATAGTGTGTCCAAAGCAGTCTTAAG 728

Qy   1143 CGAATTTGCCTGGGGAAGGGGAAATCCGTCTGGGCCACTCCTAGTTCCG 1202
          ||||||||||||||||||||||||||||||||||||||||||
Db   1709 TCAGAATCCGTACC--------------------TATTGTCAAAGCAGTCGTAAG 1674

Qy   1256 CGAATTTGCCTGGGGGCAGGGGAAATCGCTCTCGGCACTCCGTAGTTCA 1197
          ||||||||||||||||||||||||||||||||||||||||||
Db    729 AAGAGGTCCCATTACCCCACTCTTTCCGCCCTAATGGAGGTCTCCAGTTTAGGTAAATAA 788

Qy   1203 CCCCTTCAGCCTCAATGTTGTTGTTATGTGTTCGGGTTCAGTGGTTGCTTCTGCCGCC-CCCC 1261
          |||||||||||||||||||||||||||||||||||||||||
Db   1673 AAGAGGGTCCCAAATCCCCCACTCTTTCCGCCCTAATGGAGGTCTCCAGTTTCGGTAAATAT 1614

Qy   1196 CCCCTCAGCCCCAGTGTTTTGTTA---TTTTCGGGTTCAGCTTGCTTTTGCCCGGTCTCC 1140
          |||||||||||||||||||||||||||||||||||||||||
Db    789 AAGGATTGTTGGAGGTGGAGGGGAAAG------AACTACTATTTTCAAACATGCATTGCGGA 843

Qy   1262 ATCGACGCAAATCTCCACCAATCAATGGCCTGGTCGGTGTTGGGGGACCAAGTGGTGAGAGCC 1321
          |||||||||||||||||||||||||||||||||||||||||
Db   1613 AAGTAATAAGGATTGTTGGGGGTGGAGGGGAAAATAAATTATTTCCAGCATCGCGTTCCGGA 1554

Qy   1139 GTCGACGCAATCGCCACCAGTCAATGGGGTGGTCCGTTTGAGGGGACAAGTGGTAAGAGCC 1080
          |||||||||||||||||||||||||||||||||||||||||
Db    844 ACGAAAAGGCCTTGGCCACACTCGTTCCTTGGAAAACTGTAGTCTTATGGAGAGGAACATCCA 903

Qy   1322 AATCATCTTGGGCGAACACTCGGGAGCAAACAGGGGAGACTAGTTACTCTGTCTTTATCCGCCATGT 1381
          |||||||||||||||||||||||||||||||||||||||||
Db    904 ATACCAAAAGCGGGGGCACAATTCTCACGGAAATCCAGTGGATAGAGCTTCGGGG 963

Qy   1079 AATCTTCTTGGGCGAAAACCCGGAGAAAC--GGGACTAGTTACTCTCTTTGTCCCCATGT 1022
          |||||||||||||||||||||||||||||||||||||||||
Db   1553 ATGAAAAGGTCTTCGCCACCAGTGTTCCTTAGAAAACTGTAGTCTTATGGAGAGGAACATCCA 1494

Qy   1382 TAGATTCACCCCACACAGGGATAGCGGCGGGGCGAGAGCCGGTAGCGGAGCGGTCCTTG 1431
          |||||||||||||||||||||||||||||||||||||
Db    904 ATACCAAAAGCGGGGGCACAATTCTCACGGAAATCCAGTGGATAGAGCTTCGGGG 963

Qy   1021 TAGATTCACCCCACAGAGATAGCGCGGACAGAGACTGGCCAGCGGACGGGTCTTTG 972
          |||||||||||||||||||||||||||||||||||||
Db   1493 ATACCAGAGGCGGGGGGACACAATTCTCACGGATAGAATTAGAATTGGGAACCTGTTGCCCG 1434
```

GENERAL INFORMATION:

RESULT 10
US-09-949-016-12668/c
Sequence 12668, Application US/0994901б
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12668
LENGTH: 85152
TYPE: DNA
ORGANISM: Human
US-09-949-016-12668

Query Match 49.2%;   Score 703.6; DB 3; Length 85152;
Best Local Similarity 85.0%;   Pred. No. 1e-210;
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

```
Qy    381 CACAGTTTTAATTTATCTGTAATTCCCACGCTTACTGTTGCCACGGAA---------------- 429
          |||||||||||||||||||||||||||||||||||||||||
Db   2009 CGCAGTTTTAATTTATTCTGTAATTCCCGCGGCTTTTCCGTTGCCACGGAAACCAAGGGGCT 1950

Qy    430 ACCGGCTGAGCAATAGCCTCTCAGAATAGCACAGTTCAGAGGAGGGCGGGA 489
          |||||||||||||||||||||||||||||||||||||||||
Db   1949 ACGGGCTAAGCAGCAGCCTTCAGAATACGAAAATCAAAGTTACAATCAGAGTGTTGGGATATAT 1890

Qy    490 CAGAAGAGACCTAGCACATCTCTCGGGGCCTCGTGGGGTTGGCCACCCAGTCCTCCCCTGG-TGA 548
          |||||||||||||||||||||||||||||||||||||||||
Db   1889 CAGAAAGAGCCAAGCGGTCTCTCCGGGGCTCTGGATTGGCCACCCAGTCCTGCCCCGGATGA 1830

Qy    549 CATAAAAAAGAGAGACGGAAAAACGGAAGNAGAGATTCTACCTGAGTTCGCCGGTAAACGCGCCCGC 608
          |||||||||||||||||||||||||||||||||||||||||
Db   1829 CGTAAAAAGGAAAAAGAGACGGAAGAGGAAAGAATTCTACCTGAGTTTGCCATAAAAGTGCCCTGC 1770

Qy    609 CCTCTGCCTCTAGCGGCTTATTACGTCACAGTAATTGCTGTACCAAGG 668
          |||||||||||||||||||||||||||||||||||||||||
Db   1769 CCTCTAGCCTTCTACTCTTCCAGTTGCGGGCTTATTGGCATCACAGTAATTGCTACGGAAGG 1710
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RESULT 11
US-09-023-655-887/c
Sequence 887, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/023,655
  FILING DATE: HEREWITH
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
  FILING DATE:
  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
  NAME: Zeller, Karen J.
  REGISTRATION NUMBER: 37,071
  REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (650) 855-0555
  TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 887:
SEQUENCE CHARACTERISTICS:
  LENGTH: 3798 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
IMMEDIATE SOURCE:
  LIBRARY: GENBANK
  CLONE: g1147602
US-09-023-655-887:

Query Match   49.0%; Score 701; DB 3; Length 3798;
Best Local Similarity 84.9%; Pred. No. 1.1e-210;
Matches 908; Conservative 0; Mismatches 111; Indels 51; Gaps 9;

```
Qy   381 CACAGTTTTAATTTATCTGTAATTCCACGCTTTACTGTTGTTGCCACGGA---------- 429
             |||||||||||||||||||||||||||  |||||| |||||||||||||||
Db  1589 CGCAGTTTTAATTTATCTGTAATTCCCGGCTTTTCCGTTGCCACGGAAACCAAGGGGCT 1530

Qy   430 ACCGCTGAGCAATAGCCTTCAGAAATAGGAGAAATCAAGACACAGTCGAGGAAGGCGGGA 489
             ||||| |||| ||||| ||||| ||| |||| |||| ||  |||||| ||||| |||||
Db  1529 ACCGCTAAGCCAGCAGCCTCTCAGAATACGGAAATCAAAGGTACAATCAGAGGATGGGAGGGA 1470

Qy   490 CAGAAAGAGCCTAGCATCTCTCGGGGCTTCTGGGTTGGCCACCCAGTCTCTCCCTGG-TGA 548
             ||||| |||| ||| |||||||||||  |||  |||||||||||||||| |||| ||  ||
Db  1469 CAGAAGAGCCAAGCGTCTCTCGGGGCCTCTCGGATTGGCCACCCAGTCTCGCCCCGGATGA 1410

Qy   549 CATAAAAAGAAAGAGGAGAAAAGGAGAGAATTCTACCTGAGTTCGCCGTAAAGGCCCCGC 608
             | |||||| ||||| |||   |||| ||||||||||||||| | || |||||| |||||
Db  1409 CGTAAAAGGAAAGAGAGACGGAAGAATTCTACCTGAGTTTGCCATAAAAGTGCCTGC 1350

Qy   609 CCCTCGCCTCTACGGCTTCCAGTTGCGGCTTATTACGGTCACAGTAATTGCTGTACCAACG 668
             |||||  ||||||  |||||||||||  |||||| | |||||||||||||||  |||| |
Db  1349 CCCTCTAGCCTCTACTCTTCCAGTTGCCGGCTTATTGCCATCACAGTAATTGCTTACGAAGG 1290

Qy   669 TCAGAATGTGCCACCTGAGGCCCTGAAATATCAGCGTAAGAGTAGTTGTCCAAAGCCAGTTCTTAAG 728
             |||||||  |||| |        |                  |||||||||||||| || |||| |
Db  1289 TCAGAATCCTACC--------------------------TATTGTCCAAAGCAGTTCGTAAG 1254

Qy   729 AAGAGGTCCCATTACCCCACTCTTCCGCCCTAAGTGAGGGCTCCCAGTTTAGGTAAATAA 788
             ||||||||||| |||||||||||||| |||||| |||| |||| ||||||  |||| |
Db  1253 AAGAGGTCCCAATCCCCACTCTTCCCGCCCTAATGGAGGTCTCCAGTTTCGGTAAAAT 1194

Qy   789 AAGGATTGTTGGGAGGTGAGGGAAAG------AACTACTATTTCCAACATGCATTGCGA 843
             ||| ||||||||| |||||||||||      ||  | |||| |||| |||| |||| ||
Db  1193 AAGTAATAAGGATTGTTGGGGGTGAGGGAAATAAATTATATTCCAGCATGCGTTGCGGA 1134

Qy   844 ACGAAAAGCCTTGGCCCACACTGTTCCTTGGAAACTGTAGTTCTTATGGAGGAACATCCA 903
             | |||| |||| | ||||| ||||||||| ||| |||||||  |||||||||||||||||
Db  1133 ATGAAAGGTCTTCCGCCACAGTGTTCCTTAGAAAACTGTAGTCTTATGGAGGAACATCCA 1074

Qy   904 ATACCAAGCGGGGCACAATTCTCACGGAAATCAGTGGATAGAATTGGAGAGACCTCGCGGG 963
             ||||| || |||||||||||||||||||||| |||||||||| |||||||||||  |||
Db  1073 ATACCAGAGCGGGGCACAATTCTCACGGAAATCCAGTGGATAGATTGGAGAGACCTGTGCCG 1014

Qy   964 CTTATACATGTCAACAGTAATGGATTGGAGTGTTGTTAATGTTCTCCTATCTTGAGAGCAG 1023
             ||| ||| ||||||||||  ||||| ||||   ||| ||||| |  |||| || ||||||
Db  1013 CTTGTACTTGTCAACAGTTAATGGACTGGAG---TGTTATGTTGTTCGTTGTATTTGAAAGCAG 957

Qy  1024 AGACTAGGGCCAAAAAAAGAGATACCTACACTC-CTAGGAAGAGACTACGATTCCCATCCAGCC 1082
             | ||||||  | |||||||| ||| ||||| || ||| |||||||||||| |||||||||||||
Db   956 AAACTAGGCCTTAAAAAAAGATACGTACAACTCTTTAAGGGAGACTACAAATTCCCATCCAGCC 897

Qy  1083 CCACGAGTCTCGGGCGAAGTAGTCCTTCTTAAGGTCAGTCAGTGTGGCGGC 1142
             ||| |||||| ||||||||||||  ||  ||||||||||  | | || |||
Db   896 CCAGGAGTCTGGGCGAAGTAGTCTTGTAAGGTCAGTGGTCCTGCGGGGTGAGCGC 837

Qy  1143 CGAATTTGCCTGGGGGAAGGGGAAAATCCGCTCTTGGCCCACATCTGCCCACTCCTAGTTCCG 1202
             ||||||||||||||||  ||||||||| | ||| ||| |||| |||||  |||| |||||||
Db   836 CGAATTTGCCTGGGGGCCAGGGGAAAATGGCTCTGGGGCCCATGTCTGCGGCCACTCGTAGTTCCA 777

Qy  1203 CCCCTCAGCCTCAATGTTTGTTATTGTTGGGTTCAGGTTGCTTCTGCCCGCCCCG-CCCC 1261
             |||||||||| | |||||||||| |   ||  |||||||||||| ||||| | || ||||
Db   776 CCCCTCAGCCCCCAGTGTTTGTTA---TTTTTCGGGTTCAGGTTGCTTTGCCCGGTCTCC 720

Qy  1262 ATCGACGCAATCTCCACCAATCAATCAATGGCGGTGTGGTCGTTTTGAGGGACAACAAGTGGTGAGAGCC 1321
             ||||||||||| ||||| ||||||||||| | ||  ||||||||||||||||||||||||||| ||||||
Db   719 GTCGACGCAATCGCCACCAGTCAATCAATGGGGTCGTCGTTTTTGAGGGACAACAAGTGGTAAGAGCC 660

Qy  1322 AATCATCTTGGCGGAACACTCGGGAGAAACAGGGGACTAGTTACTGTCTTTATCCGCCCATGT 1381
             |||| |||||| | || || |||| ||||||   |||||||||||||||| ||| ||||||||
Db   659 AATCTTCTTGGGCGAAAACGGGGAGAAAC---GGGACTAGTTACTGTCTTGTTCGGCCATGT 602

Qy  1382 TAGATTCACCCCACAGGGATAGCGGGCGAGAGCGGGGTTAGCGCGGACGGGTCCTTG 1431
             |||||||||||||||| | |||  | || |||||| | |||   ||||| || ||||
Db   601 TAGATTCACCCCACAGAGTAGGGCGGCCCAGAGCGGCTGGGCCAGGACGGTCTTTG 552
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RESULT 12

US-09-949-016-4540/c

Sequence 4540, Application US/0994916

Patent No. 6812239

GENERAL INFORMATION:
  APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
  CURRENT APPLICATION NUMBER: US/09/949,016
  CURRENT FILING DATE: 2000-04-14
  PRIOR APPLICATION NUMBER:
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/241,755
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/237,768
  PRIOR FILING DATE: 2000-10-03
  PRIOR APPLICATION NUMBER: 60/231,498
  PRIOR FILING DATE: 2000-09-08
  NUMBER OF SEQ ID NOS: 207012
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4540
  LENGTH: 512
  TYPE: DNA
  ORGANISM: Human
US-09-949-016-4540

Query Match   19.7%; Score 281.2; DB 3; Length 512;
Best Local Similarity 91.4%; Pred. No. 2.5e-78;
Matches 299; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Qy    50 CCCCCCTCTACATTGCACGATGTGCCTCCCAAATGTTGACGTTGGCGTTGGCAGGACTTTTGCAAAC 109
             || ||| ||||||||| |||  |||||||||||||||||||||||| ||| |||||||| |||||||
Db   326 CCGGCCCCTACATTGCAGATGAGGCTCCCAAATGTTGACGTTGGCCAGGGCCTTTGCAAAC 267

Qy   110 AAGCCAGGCAAAAAGTTTCAATATTTACACTGGCTGCTGTTAATAAGGGCATTGATCTTA 169
             |||||||| ||||| | ||| ||||||||| | |||||| |||| |||| ||||||||||
Db   266 AAGCCAGGCCAAAAGGCTCAACATTTTACACCGCCGCTGCTTAATGAGGGGCATTGATCTTA 207

Qy   170 TCCTCCGTAAAGGTCACCTCATAGTCCTCGAGAATGAGGGCAGAGTAGATGCAGGCGAAGC 229
             |  ||||||||||||||| |||||  |||||||| |||||  |||||||||||||||||||
Db   266 AAGCCAGGCCAAAAGGCTCAACATTTACACCGCCGCTGCTTAATGAGGGGCATTGATCTTA 207
```

RESULT 13
US-09-880-107-2282/c
; Sequence 2282, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2282
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 M17886
US-09-880-107-2282

Query Match   19.5%; Score 279.6; DB 4; Length 512;
Best Local Similarity   91.1%; Pred. No. 8e-78;
Matches 297; Conservative   0; Mismatches 29; Indels 0; Gaps 0;

Qy   50 CCCCCCTCTACATTGCAGATGTGGCTCCCAAATGTTGACGTTGGGCTCAGGACTTTGCAAAC 109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   326 CCGGCCCCTACATTGCAGATGAGGGCTCCCAAATGTTGACGTTGGGCCAGGACCTTTGCAAAC 267

Qy   110 AAGCCAGGCCAAAAAAGTTTCAATATTTACACTGGCTGCTTTAATAAGGGCATTGATCTTA 169
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   266 AAGCCAGGCCAAAAAAGCTCAACACATTTACACCGGCTGCTTTAATGAGGGCCATTGATCTTA 207

Qy   170 TCCTCCGTAAAGGTCACCTCAATAGTCCTGCAGAATGAGGGGCAGAGTAGAATGGCAGGCAAGC 229
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   206 TCCTCCGTGACTGTCACCTCATCGTGCTGCAGAATGAGGGGCGAGTAGAATGGCAGGCGAGC 147

Qy   230 TGGGAGACGGAGGGCCATAGCGCGCGCGGGGGGGGGGCTGGGGCTCCCGGGACGGGGGTGCTA 289
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   146 TCGGAGACAGAGGGCCATGGCGCGCGGGGGGGGGGCTGGGGGGTAGGGCTGGGGCTCCCGGGACGGGGGTGCTA 87

Qy   290 CTCACCGGATGAAGTGAAGGTGAGGGTCTCACCCCAACGCGCGGCCCCTTAGCTTCCTCCGGAAGGACCGA 349
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   86 GTCGCCGGATGAAGTGAGGGCCTCACCCCAACGCAGCCCTTAGCTTCCTCCGGAAGGACCGA 27

Qy   350 ACACCTTGGCGGGCCAGGCCGAGGAAAGG 375
           |||||||||||||||||||||||||||||
Db   26 GCACCTTGGGCGGGCAGCTGAGGAAAGG 1

RESULT 14

US-09-949-016-15183
; Sequence 15183, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15183
; LENGTH: 9153
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15183

Query Match   19.5%; Score 279.4; DB 3; Length 9153;
Best Local Similarity   90.6%; Pred. No. 4.9e-77;
Matches 298; Conservative   0; Mismatches 31; Indels 0; Gaps 0;

Qy   50 CCCCCCTCTACATTGCAGATGTGGCTCCCAAATGTTGACGTTGGGCTCAGGACTTTGCAAAC 109
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2151 CCAGCCCCTACATTGCAGATGAGGGCTCCCAAATGTTGACGTTGGGCCAGGACCTTTGCAAAC 2210

Qy   110 AAGCCAGGCCAAAAAAGTTTCAATATTTACACTGGCTGCTTTAATAAGGGCATTGATCTTA 169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2211 AAGCCAGGCCAAAAAAGGTTCAACACATTTACACCGGCTGCTTTAATGAGGGCCATTGATCTTA 2270

Qy   170 TCCTCCGTAAAGGTCACCTCAATAGTCCTGCAGAATGAGGGGCAGAGTAGAATGGCAGGCAAGC 229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2271 TCCTCCGTGACTGTCACCTCATCGTGCTGCAGAATGAGGGGCGAGTAGAATGGCAGGCGAGC 2330

Qy   230 TGGGAGACGGAGGGCCATAGCGCGCGGGGGGGGGGGCTGGGGCTCCCGGGACGGGGGTGCTA 289
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2331 TTGGGAGACGGAGGGGCCATGGCACGGGCGAGTGTAGGGGCTGGGGCTCCCGGGACGGGGGTGCTA 2390

Qy   290 CTCACCGGATGAAGTGAAGGTGAGGGTCTCACCCCAACGCGCGGCCCTTAGCTTCCTCCGGAAGGACCGA 349
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2391 GTCGCAGGATGAAGTGAGGGCCCTTACCCCAACGCGCGGCCCTTAGCTTCCTCCGGAAGGACCGA 2450

Qy   350 ACACCTTGGCGGGCCAGGCCGAGGAAAGGGGT 378
           ||||||||||||||||||||||||||||||
Db   2451 GCAGCTTGGGCGGGCAGCTGAGGAAGGGGT 2479

RESULT 15
US-09-016-15546
; Sequence 15546, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15546

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;   LENGTH: 187595
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(187595)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15546

Query Match      17.4%;   Score 249.2;  DB 3;  Length 187595;
Best Local Similarity    85.3%;   Pred. No. 1e-66;
Matches  278;  Conservative   0;  Mismatches  48;  Indels   0;  Gaps   0;

Qy      50 CCCCCCTCTACATTGCAGAATGTGGGCTTCCCAAATGTTGACGTTGGGCAGGACCTTTGCAAAC 109
            ||  ||||| | |||||||||||| ||| |||||||  |||||||||||||||||||||||||
Db  172708 CCAGCCCCTACATTGTAGAATGAGGGCTCCCAAATGTTGACATTGGCCAGGGCCATTGCAAAC 172767

Qy     110 AAGGCCAGGCCAAAAAGTTTCAAATATATTTACACTGGCTGCTTTAATAAGGGGCATTGATCTTA 169
            | ||  ||||||||||||| ||||| || |||| |||||||||||||||||||||||||||||||
Db  172768 AAGCTGGACCAAAAAGGTTCAAACATTTACACCAGCTGCTTTAACGAGGGCCATTGATCTTA 172827

Qy     170 TCCTCCGTAAAGGTCACCTCATAGTCCTGCAGAATGAGGGCCAGAGTAGAATGCAGGCAAGC 229
            ||||||||| |||||||||||||||||||| |||||||| ||||||||||||||||||||||
Db  172828 TCCTTCCGTGATGGTCACCTCATTGTCATGCAAGAGTGAGGGCCTGAGTAGAATGCAGGCGAGC 172887

Qy     230 TGGGAGACGGAGGCCATAGCGCGGGCGGAGTGTTGGGGCTTGCCCGGACGCGCGGTGCTTA 289
            ||||||||| |||||| ||| ||||| |||||||||||| | ||||||||||||||||||
Db  172888 TCGGAGACAGAGGACCATGGTTATGGGGCAAGTGTGGGGCTGGCGGCTGCCCGGACGTGGTGGTA 172947

Qy     290 CTCACCGGATGAAGTGAGGGGTTCTCACCCAAACGCGGCCCTTAGCTTCCTCGGAAGGACCGA 349
            ||||||||||||||||||||||||| |||| |||||||| |||||||||||||||||||||||
Db  172948 GTTGCCCGGATGAAGTGAGGGCCTCATCCCAAACGTGGCCCTTAGCTTCCTTGGAAGGACCAA 173007

Qy     350 ACACCTTGGCGGCAGCCGAGGAAAGG 375
            |||  || ||||||||||||||||||
Db  173008 GCACTGTGGTGGCAGCTGAGGAAAGG 173033
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Search completed: August 20, 2006, 07:17:13
Job time : 304 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
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Run on: August 20, 2006, 04:46:58 ; Search time 8455 Seconds
             (without alignments)
             10823.035 Million cell updates/sec

Title: US-10-643-829-1
Perfect score: 1431
Sequence: 1 ccgtccagaacgtctcagcg..........ccggtagcggagcgccctg 1431

Scoring table: IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 3197710525 residues

Total number of hits satisfying chosen parameters: 12732272

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
       1: gb_env:*
       2: gb_pat:*
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       6: gb_ro:*
       7: gb_sts:*
       8: gb_by:*
       9: gb_un:*
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Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match Length	Match DB	ID	Description
1		1431	100.0	3800	5	HSU72483	U72483 Human 1A1.3
2		1431	100.0	147576	5	DQ190457	DQ190457 Homo sapi
3		1431	100.0	150582	5	DQ190454	DQ190454 Homo sapi
4		1431	100.0	150069	5	DQ190456	DQ190456 Homo sapi
5		1431	100.0	155470	5	DQ190455	DQ190455 Homo sapi
6		1431	100.0	156121	5	DQ190452	DQ190452 Homo sapi
7		1431	100.0	156879	5	DQ190453	DQ190453 Homo sapi
8		1431	100.0	161765	5	DQ190451	DQ190451 Homo sapi
9		1431	100.0	167910	5	DQ190450	DQ190450 Homo sapi
10		1429.4	100.0	110669	5	AC060780	AC060780 Homo sapi
11		1381	99.9	1703	5	AY581856	AY581856 Pan trogl
12		1301.8	96.5	1703	5	AY581858	AY581858 Homo sapi
13		1301.8	91.0	1706	5	AY581860	AY581860 Papio anu
14		1165.6	91.0	1688	5	AY581858	AY581858 Hylobates
15		909.4	81.5	1237	2	AR184045	AR184045 Sequence
16		727.6	50.8	1339	5	AY581855	AY581855 Pan trogl
17		727.6	50.8	80956	5	AY365046	AY365046 Pan trogl
18		722.4	50.5	81346	5	AY589042	AY589042 Gorilla g
c	19	711.2	49.7	1329	5	AY581857	AY581857 Hylobates
c	20	710.4	49.6	84982	5	AY589041	AY589041 Macaca mu
c	21	702.2	49.1	1363	5	AY581862	AY581862 Aotus tri
c	22	702	49.1	6277	2	CQ787189	CQ787189 Sequence
c	23	702	49.1	6277	2	CQ806564	CQ806564 Sequence
c	24	702	49.1	6277	2	AX795672	AX795672 Sequence
c	25	702	49.1	117143	2	CQ776448	CQ776448 Sequence
c	26	702	49.1	117143	2	AX795672	AX795672 Sequence
c	27	702	49.1	150472	5	AC135721	AC135721 Homo sapien
c	28	701	49.0	3798	2	AR380342	AR380342 Sequence
c	29	701	49.0	3798	2	HSU37574	U37574 Human BRCA1
c	30	676.8	47.3	82899	5	AY581859	AY581859 Papio anu
c	31	675.2	47.2	1357	5	AY581861	AY581861 Saguinus
c	32	637.8	44.6	1317	5	AY273801	AY273801 Rhinoloph
c	33	515.4	36.0	174483	12	AC175025	AC175025 Rhinoloph
c	34	512	36.0	4118	5	HSU77841	U77841 Human BRCA1
c	35	502.6	35.8	586	5	AC175019	AC175019 Loxodonta
c	36	494.4	35.1	143790	12	AC174860	AC174860 Sus scrof
c	37	474.4	34.5	152765	12	AC138235	AC138235 Homo sapi
c	38	450	33.2	109876	12	AF227189	AF227189 Homo sapi
c	39	450	31.4	4756	2	BD186260	BD186260 STAT6 act
c	40	446.6	31.2	155192	12	AC172475	AC172475 Bos tauru
c	41	446.6	31.2	223246	12	AC168285	AC168285 Bos tauru
c	42	446.6	31.1	111893	12	AC174864	AC174864 Dasypus n
c	43	445.2	31.0	178489	12	AC174852	AC174852 Oryctolag
c	44	443.4	31.0	178484	12	AC175004	AC175004 Oryctolag
c	45	413	28.9	6121	2	AX343496	AX343496 Sequence

ALIGNMENTS

RESULT 1
HSU72483/c

LOCUS   HSU72483   3800 bp   DNA   linear   PRI 22-DEC-1997
DEFINITION Human 1A1.3B gene, promoter region.
ACCESSION   U72483
VERSION   U72483.1 GI:1771979
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 3800)
  AUTHORS   Barker,D.F., Liu,X. and Almeida,E.R.
  TITLE   The BRCA1 and 1A1.3B promoters are parallel elements of a genomic
            duplication at 17q21
  JOURNAL   Genomics 38 (2), 215-222 (1996)
  PUBMED   8954804
REFERENCE   2 (bases 1 to 3800)
  AUTHORS   Liu,X. and Barker,D.F.
  TITLE   Direct Submission
  JOURNAL   Submitted (24-SEP-1996) Physiology, University of Utah, 410 Chipeta
            Way, Room 156, Salt Lake City, UT 84108, USA
FEATURES   Location/Qualifiers
     source   1..3800
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="17"
                     /map="17q21"
     gene   1..3800
                     /gene="1A1.3B"
     promoter   1..3800
                     /gene="1A1.3B"
ORIGIN

Query Match   100.0%;   Score 1431;   DB 5;   Length 3800;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1431;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 CCGTCCAGAACGTCTCAGCGAGCTCACGGAGCGCGCAGTCACGTTTTTTCCCCCCTCTAC 60

```
Qy   1720 CCGTCCAGAGAACGTCCTCAGCCGAGCTCAGCGACGGCAGTCACGACGTTTTTTCCCCCCCTCTAC 1661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 CCCCACGAGTCTCGGGCAAGTAGTCCTCTAAGGTCAGTGGCCTGCGGGGACGCAGTGGGGC 581

Qy   1660 ATTGCAGATGTGGGCTTCCCAATGTTGACGTTGGCTCAGGAAACAAAGCCAGGCCA 1601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCCGAAATTTGCCTCGGGGAAGGGGGAAATCCGCTCTGGCCACACTCCTAGTTC 1200

Qy   1600 AAAAGTTTCAATTACTGGCTGCTTTAATAAAGGGCAATTGATCTTTATCCTTCGGTAAA 1541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 GCCGAAATTTGCCTCGGGGAAGGGGGAAAATCCGCTCTGGCCACATCTGGCCACTCCTAGTTC 521

Qy    181 GGTCACCTCATAGTTCCTGCAGAATGAGGCCAGAGTGCCGCAAGCTGGGAGGACGGA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CGCCCCTCAGCCTCAATGTTGTTATTGTTCGGTTCAGGTTTCCGGTTCAGTTTCGGTTT 1260

Qy   1540 GGTCACCTCATAGTTCCTGCAGAATGAGGCCAGAGTGATGCAGCAAGCTGGGAGGACGGA 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 CATCGGACGGCAATCTCCACCAATCAATCAATGGCGGTGTCGTTTGGAGGGACCAGGACGGA 1320

Qy    241 GGCCATAGTGCGCGGGAGTGTGGGGGGCTCGGGGGCGGAGTGTGGGGCGGAAGCTGGGGACATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460 CATCGGACGGCAATCTCCACCAATCAAATGCGGGTGGTCGTTTTGAGCGACAAGTGGTGAGAGC 401

Qy   1480 GGCCATAGGCGGGGGCGAGTGTGGGGCTGCGGGGGCTGGGGGCTCGGGGGCTGGGGCGCAGTGGGGCATG 1421
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Db   1321 CAATCATCTTGGGGAAACACTCCGGGAGAAAACAGGGGGACTAGTTACTGTTCTTTATCCGGCCATG 1380

Qy    301 AAGTGAGAGGGTCTCACCCACAGCGGGCCCTTAGCTTCCTCCGGAAGGACACACCTTGGCG 360
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Db   1381 TTAGATTCACCCCACACAGGGATAGCCGCAGAGCCCGGTAGCCGGACGGTCCTTG 1431

Qy   1420 GCAGCCACGACGAAGGGGTTCCACAGTTTTAATTTATCTGTAATTCCCACGGCTTTACTGTT 1420
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Db    340 TTAGATTCACCCCACAGGGATAGCCGCAGAGCCCGGTAGCCGGACGGTCCTTG 290
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RESULT 2

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DQ190457/c

LOCUS       DQ190457      147576 bp    DNA     linear   PRI 24-SEP-2005
DEFINITION  Homo sapiens clone mck41_A neighbor of BRCA1 gene 1 (NBR1) gene,
            partial cds; hypothetical protein LOC10230 (NBR2) gene, complete
            cds; and breast cancer 1 early onset (BRCA1) gene, partial cds.
ACCESSION   DQ190457
VERSION     DQ190457.1  GI:75875128
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 147576)
  AUTHORS   Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y.,
            Haugen,E., Kaul,R. and Olson,M.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2005) Genome Center, Department of Medicine,
            University of Washington, Box 352145, Seattle, WA 98195, USA
FEATURES             Location/Qualifiers
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                     /chromosome="17"
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ORIGIN

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	Query Match	Best Local Similarity　100.0%;　Score 1431;　DB 5;　Length 147576;	
	Matches 1431;　Conservative　0.0%;　Pred. No. 0;　Mismatches　0;　Indels　0;　Gaps　0;		

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Qy       1  CCGGTCCCAGAAGCGTCTCAGCGGAGCTCACCGACGCGCAGTCACGTTTTTTCCCCCTTCTAC   60
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Db   24786  CCGGTCCCAGAAGCGTCTCAGCGGAGCTCACCGACGCGCAGTCACGTTTTTTTCCCCCTTCTAC   24727

Qy      61  ATTGCAGATGTGGCTCCCCAAATGTTGACGTTGGCCAGGACCTTTGCCAAACAAGCCAGGCCA   120
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Db   24726  ATTGCAGATGTGGCTCCCCAAATGTTGACGTTGGCCAGGACCTTTGCCAAACAAGCCAGGCCA   24667

Qy     121  AAAAGTTTCAAATATTTACACTGGCTTGCTTTAATTAAGGGCCATTGACTCTTATCCTTCGTAAA   180
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Db   24666  AAAAGTTTCAAATATTTACACTGGCTGCTTTAATTAAGGGCCATTGACTCTTATCCTTCGTAAA   24607

Qy     181  GGTCACCTCATTAGTTCCTGCAGAATGAGAGGCCAGAGTAGATGCAGCCAAGCTTCACCGGATG   240
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Db   24606  GGTCACCTCATTAGTTCCTGCAGAATGAGAGGCCAGAGTAGATGCAGCCAAGCTTCACCGGATG   24547

Qy     241  GGCCATAGGCGGGCGGAGTGTGGGGGCTGGGGACGGCGGTGCTACTCACCGGATG   300
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Db   24546  GGCCATAGGCGGGCGGAGTGTGGGGGCTGGGGACGGCGGTGCTACTCACCGGATG   24487

Qy     301  AAGTGAGGGTCTCACCCCAAACGCGGCGCCTTGACTCCTCTCCGGAAGGACCGGGCGGA   360
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Qy     361  GCAGCCGAGGAAAGGGGTTCCACAGTTTAATTTATCTGTAATTCCCACGCTTTACTGTT   420
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Qy     481  AGGGGCGGGACAGAAAGAGCCTAGCATTCTTCGGGGTTGGGCCTCGGGGTGGGCACCCAGTCCTC   540
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Qy     541  CCTGGGTGACATAAAAGGAGAAAGAGAAAGGAGAGAAGGAGAGAATTCTACCTGAGTTCGGCGTAAA   600
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Db   24006  GTAAATAAAAGGATTGTTGGGAGGTGGAGGGAAGAACTACTATTTCCAACATGCATTGC   23947

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RESULT 3
DQ190454/c

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Qy  1081 CCCCACGAGTCTCGGGCCAGTAGTCCTTCTTAGGTGGTGGCCACGACGCAGTGGGC 1140
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Db 23706 CCCCACGAGTCTCGGGCCAGTAGTCCTTCTTAGGTGGTGGCCACGACGCAGTGGGC 23647

Qy  1141 GCCGAATTTCGCCTGGGGAGGGAAATCCGGTTCGGTTCTCTGGCCCCACGCCCACTCCACGTTC 1200
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Db 23466 CAATCATCTTGGGCGAACACTCGGGAGAACAGGGGACTAGTTACTGTCTTTTATCCGCCATG 23407

Qy  1381 TTAGATTCACCCACAGGGATAGCGGCGAGCCGGACGGGTCCTTG 1431
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ACCESSION   DQ190454
VERSION   DQ190454.1 GI:7587470
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 150582)
  AUTHORS   Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y.,
            Haugen,E., Kaul,R. and Olson,M.V.
  TITLE   Direct Submission
  JOURNAL   Submitted (01-SEP-2005) Genome Center, Department of Medicine,
            University of Washington, Box 352145, Seattle, WA 98195, USA
FEATURES   Location/Qualifiers
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DEFINITION Homo sapiens clone mck43_A neighbor of BRCA1 gene 1 (NBR1) gene,
            partial cds; and hypothetical protein LOC10230 (NBR2) and breast
            cancer 1 early onset (BRCA1) genes, complete cds.
LOCUS   DQ190454   150582 bp   DNA   linear   PRI 24-SEP-2005
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                     LLQNPYRIPPLPFIKSFVKTKCKKNLLEENFEEHSMSPEREMGNENIPSTVSISRNN
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                     LQPEVYKQSLPGSNCKHPEIKKQEYEEVVQTVNTDFSFYLISDNLEQPMGSHASOVC
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                     LRNSLNDCSNQVILAKASQEHHLSEETKCSASLFSSQCSELEDLTANTNTQDPFLIGS
                     SKQMRHQSESQVGLSDKELVSDDEERGTGLEENNQEEQSMDSNLGEAASGCSETSV
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ORIGIN
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Query Match
Best Local Similarity   100.0%;   Score 1431;   DB 5;   Length 150582;
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Matches 1431;   Conservative   0;

Qy       1 CCGTCCAGAACGTCTCAGCGACGACGAGCTCACGCAGCTACGTTTTTTTCCCCCTCTAC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20243 CCGTCCAGAACGTCTCAGCGACGACGAGCTCACGCAGCTACGTTTTTTTCCCCCTCTAC 20184

Qy      61 ATTGCAGAGATGTGGCTCCCAATGTTGACGTTGGCCAGGACCTTTCCAAACAAGCCAGGCCA 120
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Db   20183 ATTGCAGAGATGTGGCTCCCAATGTTGACGTTGGCCAGGACCTTTCCAAACAAGCCAGGCCA 20124

Qy     121 AAAAGTTTCAATATTTACACTGGGGCATTGAATCTTATCCTCCGTAAA 180
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Db   20123 AAAAGTTTCAATATTTACACTGGGGCATTGAATCTTATCCTCCGTAAA 20064

Qy     181 GGTCACCTCATAGTCCTGCAGAATGAGGGCGCAGCAGTGGGGGAGACGGA 240
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Db   20063 GGTCACCTCATAGTCCTGCAGAATGAGGGCGCAGCAGTGGGGGAGACGGA 20004

Qy     241 GGCCATAGCGCGGCGGGAGTGTGGGGGGCTGCCGGCGCTACTCACCGGATG 300
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Db   20003 GGCCATAGCGCGGCGGGAGTGTGGGGGGCTGCCGGCGCTACTCACCGGATG 19944

Qy     301 AAGTGAGGGTCTCACCCCAAGCGGGGCCTTAGCTTCCTCCGGAAGGACCAACACCTTGCG 360
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Db   19943 AAGTGAGGGTCTCACCCCAAGCGGGGCCTTAGCTTCCTCCGGAAGGACCAACACCTTGCG 19884

Qy     361 GCAGCCGGAGGGAAAGGGGGTTCCACACGTTTAATTTATCTGTAATTCCCACGCTTTACTGTT 420
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Db   19883 GCAGCCGGAGGGAAAGGGGGTTCCACACGTTTAATTTATCTGTAATTCCCACGCTTTACTGTT 19824

Qy     421 GCCACGCGAAACCGCTGAGCCAATAGCCTCTCAGAATAGGAAATCAAGACACTCAGACTCAGAGGA 480
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Db   19823 GCCACGCGAAACCGCTGAGCCAATAGCCTCTCAGAATAGGAAATCAAGACACTCAGACTCAGAGGA 19764

Qy     481 AGGGCGGGACAGAAGAGCCTAGCACTCTCTCGGGGGCTCTGGGGTTGGCCACCCAGTCCTCC 540
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Db   19763 AGGGCGGGACAGAAGAGCCTAGCACTCTCTCGGGGGCTCTGGGGTTGGCCACCCAGTCCTCC 19704

Qy     541 CCTGGTGACATAAAAAGGAAGAGACAGGAAAAAGGAGAATTCTACCTGAGTTGCGGCGTAAA 600
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Db   19703 CCTGGTGACATAAAAAGGAAGAGACAGGAAAAAGGAGAATTCTACCTGAGTTGCGGCGTAAA 19644

Qy     601 GGCCCCGCCCCTCTCGCCTCTAGGCTTCCAGTTGCGGCTTATTACGTCACAGTAATTGCTG 660
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Db   19643 GGCCCCGCCCCTCTCGCCTCTAGGCTTCCAGTTGCGGCTTATTACGTCACAGTAATTGCTG 19584

Qy     661 TACCAAGGTCAGAAATCGGCCACTGAGGCCTGAATATCAGCGTGAAGATAGTAGTGTCCAAAGCA 720
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Db   19583 TACCAAGGTCAGAAATCGGCCACTGAGGCCTGAATATCAGCGTGAAGATAGTAGTGTCCAAAGCA 19524

Qy     721 GTCTTAAGGAAGAGGTCCCATTACCCCACCACTCTTCTTCCGCCTCTTCTCCAGTTTAG 780
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Db   19523 GTCTTAAGGAAGAGGTCCCATTACCCCACCACTCTTCTTCCGCCTCTTCTCCAGTTTAG 19464

Qy     781 GTAAAATAAAAGGATTGTTGGGAGGTGGGAGAGAACTACTATTTTCCAACATGCATTGC 840
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Db   19463 GTAAAATAAAAGGATTGTTGGGAGGTGGGAGAGAACTACTATTTTCCAACATGCATTGC 19404

Qy     841 GGAACGAAAGGCCTTGGCCACACTGTTCCTTGGGAAACTGTAGTCTTTATGGAGGAGGAACAT 900
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Db   19403 GGAACGAAAGGCCTTGGCCACACTGTTCCTTGGGAAACTGTAGTCTTTATGGAGGAGGAACAT 19344

Qy     901 CCAATACCAAAGCGGCCACAATTCTCACGGAAATCCAGTGGATAGAATTGGAGACCTCCGC 960
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Db   19343 CCAATACCAAAGCGGCCACAATTCTCACGGAAATCCAGTGGATAGAATTGGAGACCTCCGC 19284

Qy     961 GGGCTTATACATGTCAACAGTAATGGATTGGAGTGTTGGTTATTGTCTCCTATACTTGAGAG 1020
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Db   19283 GGGCTTATACATGTCAACAGTAATGGATTGGAGTGTTGGTTATTGTCTCCTATACTTGAGAG 19224

Qy    1021 CAGAGACTAGGCCAAAAAAGATACCTACAACTCCTACAACTCCTAGGAGGAGGACTACGATTCCATCCAG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   19223 CAGAGACTAGGCCAAAAAAGATACCTACAACTCCTACAACTCCTAGGAGGAGGACTACGATTCCATCCAG 19164

Qy    1081 CCCCACGAGTCTCGGGCACAGTAGTCGTCGCTCTAAGGTCAGTGGCCTGCGCGGGAGCCAGCAGTGGGC 1140
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Db   19163 CCCCACGAGTCTCGGGCACAGTAGTCGTCGCTCTAAGGTCAGTGGCCTGCGCGGGAGCCAGCAGTGGGC 19104

Qy    1141 GCCGAATTTGCCTGGGGAGGGAGAAATCCCGCTCTGCGGCCATCTGCCGCCACTCCTAGTTC 1200
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Db   19103 GCCGAATTTGCCTGGGGAGGGAGAAATCCCGCTCTGCGGCCATCTGCCGCCACTCCTAGTTC 19044

Qy    1201 CGCCCCCTCAGCCTCAAGTGTTGTTTATTGGTTTGTGTTCAGGTTGTTCTTCTGCCCGCCCC 1260
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Db   19043 CGCCCCCTCAGCCTCAAGTGTTGTTTATTGGTTTGTGTTCAGGTTGTTCTTCTGCCCGCCCC 18984

Qy    1261 CATCGACGCGAATCTCCCACAAATCAAATGGCCGTGGGTCGTTTTTGAGGGACAAGTGAGAGC 1320
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Db   18983 CATCGACGCGAATCTCCCACAAATCAAATGGCCGTGGGTCGTTTTTGAGGGACAAGTGAGAGC 18924

Qy    1321 CAATCATCTTGGGCAAACACTCGGAGAAACAGGGGACTAGTTACTGTCTTTATCTTTATCCCGCCATG 1380
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Db   18923 CAATCATCTTGGGCAAACACTCGGAGAAACAGGGGACTAGTTACTGTCTTTATCTTTATCCCGCCATG 18864

Qy    1381 TTAGATTCACCCCACCAGGGGATAGCGGCCAGAGCCCGGTAGCCGGACACGGTTCCTTG 1431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18863 TTAGATTCACCCCACCAGGGGATAGCGGCCAGAGCCCGGTAGCCGGACACGGTTCCTTG 18813
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RESULT 4

DQ190456/c

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LOCUS       DQ190456             150669 bp    DNA     linear   PRI 24-SEP-2005
DEFINITION  Homo sapiens clone mck578 U neighbor of BRCA1 gene 1 (NBR1) gene,
            partial cds; and hypothetical protein LOC10230 (NBR2) and breast
            cancer 1 early onset (BRCA1) genes, complete cds.
ACCESSION   DQ190456
VERSION     DQ190456.1  GI:75875068
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 150669)
  AUTHORS   Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y.,
            Haugen,E., Kaul,R. and Olson,M.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2005) Genome Center, Department of Medicine,
            University of Washington, Box 352145, Seattle, WA 98195, USA
FEATURES             Location/Qualifiers
     source          1..150669
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="17"
                     /clone="mck578 U"
     gene            complement(<142..>18852)
                     /gene="NBR1"
     mRNA            complement(join(<142..291,1003..1293,1388..1547,
                     3061..3270,3866..4033,4840..5054,5523..5600,8198..8392,
                     13831..13853,15236..15254,16650..16712,18751..18852))
                     /gene="NBR1"
                     /product="neighbor of BRCA1 gene 1"
     CDS             complement(join(<142..291,1003..1293,1388..1547,
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                     /codon_start=1
                     /product="neighbor of BRCA1 gene 1"
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                     /translation="MBPQVTLNVTFKNEIQSFLVSDPENTTWADIBAMVKVSPDLNTI
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mRNA            complement(<54686..>55917)
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gene            complement(join(54686..54841,55735..>55917))
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CDS             complement(join(54686..54841,55735..>55917))
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                /note="neighbor of BRCA1 gene 2"
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                /protein_id="ABA29227.1"
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                GVPSFLTSSILWKSAVFABDNGLKIHLCSYRQDDLVLFYDCTSFVLTFGPSPWFLTQ
                GFLNPLEFSA"
gene            <70561..>148986
                /gene="BRCA1"
mRNA            join(<70561..70640,78878..78931,80125..88125,88202,89702..89790,
                90397..90536,94779..94884,97370..97415,98738..98814,
                99800..103225,103628..103716..112085..112256,
                118047..118173,120140..120330,123423..123733,
                126968..127055,130712..130789,131290..131310,
                137528..137611,143546..143600,145469..145542,
                146960..147020,148862..148986)
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                /product="breast cancer 1 early onset"
CDS             join(70561..70640,78878..78931,80125..88125,88202,89702..89790,
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                118047..118173,120140..120330,123423..123733,
                126968..127055,130712..130789,131290..131330,
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ORIGIN

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Db 24822  CCGTCCAGAACGTCTCAGCGAGCTCACGACGGCGCAGTCAGGTTTTTTTCCCCCTCTAC  24763
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Db  23922  CCAATACCAAAAGCGGGCACAAATTCTCACGGAAATCCAGTGGATAGATTGGAGACTTCCGC  23863

Qy    961  GGGCTTATACATGTCAACAGTAATGGATTGGAGTGTTGTTAGTTCTCCTATCTTGAGAG  1020
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Db  23862  GGGCTTATACATGTCAACAGTAATGGATTGGAGTGTTGTTAGTTCTCCTATCTTGAGAG  23803

Qy   1021  CAGAGACTAGGCCAAAAAAAGATACCTACAACTCCTAGGAAGACTACGATTCCCATCCAG  1080
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Db  23802  CAGAGACTAGGCCAAAAAAAGATACCTACAACTCCTAGGAAGACTACGATTCCCATCCAG  23743

Qy   1081  CCCCACGAGTCTCGGGCAAGTAGTCCTCTAAGGTCAGTGGCCTGGGCCGGCAGTGGGC  1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23742  CCCCACGAGTCTCGGGCAAGTAGTCCTCTAAGGTCAGTGGCCTGGGCCGGCAGTGGGC  23683

Qy   1141  GCCGAATTTGCCTGGGGAAGGGGGAAATCCGCTCTGGCCCCACATCTGCCACTCCCTAGTTC  1200
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Db  23682  GCCGAATTTGCCTGGGGAAGGGGGAAATCCGCTCTGGCCCCACATCTGCCACTCCCTAGTTC  23623

Qy   1201  CGGCCCCTCAGCCTCAATGTTTGTTATTGTTGTTCGGGGTTCAGGTTGCTTCTTGCCCCGCC  1260
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Db  23622  CGGCCCCTCAGCCTCAATGTTTGTTATTGTTGTTCGGGGTTCAGGTTGCTTCTTGCCCCGCC  23563

Qy   1261  CATCGGACGGCAAATCTCCACCAAATCAATGCGCTGGTTCGTTGTTTTGAGGGACAAGTGGTGAGAGC  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23562  CATCGGACGGCAAATCTCCACCAAATCAATGCGCTGGTTCGTTGTTTTGAGGGACAAGTGGTGAGAGC  23503

Qy   1321  CAATCATCTTGGCGAACACTCGGAGAAACAGGGGACTAGTTACTGTCTTTATCCGCCATG  1380
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Db  23502  CAATCATCTTGGCGAACACTCGGAGAAACAGGGGACTAGTTACTGTCTTTATCCGCCATG  23443

Qy   1381  TTAGATTCACCCCACAGGGATAGCGGCAGAGCCGGTACGGGACGGGTCCTTG  1431
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Db  23442  TTAGATTCACCCCACAGGGATAGCGGCAGAGCCGGTACGGGACGGGTCCTTG  23392
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RESULT 5

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LOCUS       DQ190455               155470 bp    DNA     linear   PRI 24-SEP-2005
DEFINITION  Homo sapiens clone mck554_A neighbor of BRCA1 gene 1 (NBR1) gene,
            partial cds; and hypothetical protein LOC10230 (NBR2) and breast
            cancer 1 early onset (BRCA1) genes, complete cds.
ACCESSION   DQ190455
VERSION     DQ190455.1  GI:75874960
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 155470)
  AUTHORS   Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y.,
            Haugen,E., Kaul,R. and Olson,M.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2005) Genome Center, Department of Medicine,
            University of Washington, Box 352145, Seattle, WA 98195, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="17"
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     CDS             complement(join(<2177..2252,2717..2866,3578..3868,
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                     LEGTYTSHWRLSHKGQQPGPRVWCSIIVDPFPSESSPDNIEKGMISSSKTDDLTCOQE
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ORIGIN
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Qy   301  AAGTGAGGGGTCTCACCCCAACGGGGCGCCTTAGCTTCCTCCGGACGGACCCGAAACACCTTGGCG   360
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Db 27091  AAGTGAGGGGTCTCACCCCAACGGGGCGCCTTAGCTTCCTCCGGACGGACCCGAAACACCTTGGCG 27032

Qy   361  GCAGCCGAGGAAGGGTTCCACAGTTTTAATTATTCTGTAATTCCACGCTTTACTGTT   420
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Qy   541  CCTGGGTGACATAAAAAGAAGAGACGGAAAAGGAAGAATTCTACCTGAGTTGCCCGTAAA   600
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Qy   601  GCGCCCGCCCCTCTTCGCCTTCAGTTCCGGCTTCACGGTTGGGCGGCTTATTACGTTACGTTACTTGCTG   660
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Qy   661  TACCAAGGTCAGAAATGCCACTGACCGCTGAATATCAGCGTAAGATAGTGTCCAAAGCA   720
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Qy   781  GTAAATAAAAGGATTGTTGGGAGGTGGAGGGAGGAAAAGAACACTACTATTTCCAACATGCATTGC   840
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Db 26611  GTAAATAAAAGGATTGTTGGGAGGTGGAGGGAGGAAAAGAACACTACTATTTCCAACATGCATTGC 26552

Qy   841  GGAACGGAAAGGCCTTGGCCACCACTGTTCCTTGGGAAACTGTAGTCTTAATGGAGAGGAACAT   900
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Qy   961  GGGGCTTTATACATGTCAAACAGTAATGGAGTTGGGAGTGTTGTTAATGGAGACCTCCGC  1020
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Qy  1261  CATCGGACGGAATCTTCCACCAAATCAAATGCGGTCGTCGTTTTGAGGGGACAAGGTGGTGGGAGC  1320
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            cancer 1 early onset (BRCA1) genes, complete cds.
ACCESSION   DQ190452
VERSION     DQ190452.1  GI:75874674
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 156121)
  AUTHORS   Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y.,
            Haugen,E., Kaul,R. and Olson,M.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2005) Genome Center, Department of Medicine,
            University of Washington, Box 352145, Seattle, WA 98195, USA
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ORIGIN

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        Matches 1431;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db      23801 CCGTCCAGAACGTCTCAGCGAAGCTCACGACGGCGCAGTCACGTTTTTTTCCCCCTCTAC 23742

Qy         61 ATTGCAGATGTGGCTCCCCAATGTTGACGTTGGCCAGGACCTTTGCAAAACAAGCCAGGCCA 120
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Qy        121 AAAAGTTTCAAATATTACACTGGGTCTGCTTAATAAGGAGCAATTGATCTTATCCTCGGTAAA 180
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Db      23681 AAAAGTTTCAAATATTACACTGGGTCTGCTTAATAAGGAGCAATTGATCTTATCCTCGGTAAA 23622

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Qy        241 GGCCATAGCGCGCGGAGCGAGTGTGGGCGGCTGGGGCTGCCGGACGCGCGGCGGATG 300
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Qy        301 AAGTGAGGGGTCTCACCCCAACGCGGGCCTTAGCTTCCTCGGAAGGACCGGAACACCTTGGCG 360
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RESULT 9

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DEFINITION Homo sapiens clone mck432_A neighbor of BRCA1 gene 1 (NBR1) gene,
            partial cds, and hypothetical protein LOC10230 (NBR2) and breast
            cancer 1 early onset (BRCA1) genes, complete cds.
ACCESSION   DQ190450
VERSION   DQ190450.1 GI:75874526
KEYWORDS   .
SOURCE   Homo sapiens (human)
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo
REFERENCE   1 (bases 1 to 167910)
  AUTHORS   Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y.,
            Haugen,E., Kaul,R. and Olson,M.V.
  TITLE   Direct Submission
  JOURNAL   Submitted (01-SEP-2005) Genome Center, Department of Medicine,
            University of Washington, Box 352145, Seattle, WA 98195, USA
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Qy   541 CCTGGTGACATAAAAAGAGAATAGGGGAAAGTTCTACCTGAGTTCGCCGTAAA 600
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ORIGIN

Query Match          100.0%;  Score 1431;  DB 5;  Length 167910;
Best Local Similarity 100.0%;
Matches 1431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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RESULT 10
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DEFINITION  Homo sapiens chromosome 17, clone RP11-242D8, complete sequence.
ACCESSION   AC060780
VERSION     AC060780.18  GI:29126449
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
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            Hominidae; Homo.
REFERENCE   1  (bases 1 to 110669)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-242D8
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 110669)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,P.,
            Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Donino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,I., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McBwan,P., McGurk,A., McKernan,K., McPheeters,R.,
            Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,D., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 110669)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
            Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
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            Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
            Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 110669)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
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            Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   5  (bases 1 to 110669)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
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            Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
            Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
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            Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
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            Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
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            Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
            Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 20, 2003 this sequence version replaced gi:24496797.
            All repeats were identified using RepeatMasker.
            The remainder overlaps accession number AC109326 [WICGR project
            L24004].
            Only the first 110.7 kilobases of this clone are being submitted.
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            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
            Center project name: L7945
            Center clone name: 242_D_8
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     repeat_region   720..763
                     /rpt_family="L2"
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complement(15235..15526)

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db   84323 CCGTCCAGAACGTCTCAGCGAGCTCACGAACGCGCAGTCACGTTTTTTTCCCCCCCCTAC 84382

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Db   84443 AAAAGTTTCAATATTTACACTGGCTGCTTAATAAGGCGCATTGATCTCTTATCCTCCGTAAA 84502

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Db   85103 GTAAATAAAAAAGGAATTGTTGGGAGGGTGGAGGGAAAGGAGAACTACTACTATTTCAAACATGCATTGC
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Db   85163 GGAACGAAAAGGCCTTGGCCACACTGTTCCTTGGGAAACTGTAGTCTTATGGAGAGAAACAT
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Db   85223 CCAATACCAAAAGCGGGGCACAAATTCTCACGGAAAATCCAGTGGATAGATTGGAGACCTCGC
Qy   901 CCAATACCAAAAGCGGGGCACAAATTCTCACGGAAAATCCAGTGGATAGATTGGAGACCTCGC   960

Db   85283 GGGCTTATACATGTCAACAGTAAATGGAATGGAGTGTTGTTATGTTCTCCTATCTTGAGAG
Qy   961 GGGCTTATACATGTCAACAGTAAATGGAATGGAGTGTTGTTATGTTCTCCTATCTTGAGAG   1020

Db   85343 CAGAGACTAGGCCAAAAAAAAGAATAACCTACACAACTCCCTAGGAAGACTACGATTCCCATCCAG
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Db   85403 CCCCACGAGTCTCGGGCAAGTAGTCCTTAAGGTCAGTGGCCTCGCGGGACACGCAGTGGGGC
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Db   85463 GCCGAATTTGCCTCGGGGAAGGGGAGAAATCCGGCTCTGGCCCACATCTGCGCACTCCTAGTTC
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RESULT 11
LOCUS       AY581856                1703 bp    DNA     linear   PRI 13-NOV-2004
DEFINITION  Pan troglodytes BRCA1 pseudogene, NBR1 testis isoform-like, and
            NBR1 general isoform-like genes, complete sequence.
ACCESSION   AY581856
VERSION     AY581856.1  GI:51104368
KEYWORDS    .
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 1703)
  AUTHORS   Jin,H., Selfe,J., Whitehouse,C., Morris,J.R., Solomon,E. and
            Roberts,R.G.
  TITLE     Structural evolution of the BRCA1 genomic region in primates
  JOURNAL   Genomics 84 (6), 1071-1082 (2004)
  PUBMED    15537724
REFERENCE   2  (bases 1 to 1703)
  AUTHORS   Roberts,R.G., Selfe,J., Jin,H., Whitehouse,C. and Solomon,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-2004) Division of Medical and Molecular Genetics,
            GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London
            SE1 9RT, UK
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ORIGIN
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Matches 1407;  Conservative 2;  Mismatches 22;  Indels 4;  Gaps 1;

Qy      1261 CATCGCACGCAATCTCCACCAATCATGCATGGCGTGGTCGTTTTGAGGGACCAAGTGGTGAGAGC 1320
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Qy        57 CTACATTGCAGAGTGTGGCCTCCCAATGTTGACGTTGGCCAGAGACCTTGCAAACAAGCCAG 116
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Db      1023 TTCGGGACAGAAAAGGCCCTTGGCCACACTGTTCCTTTGGAAAACTGTAGTTCTTATGGGAGGA 1082

Qy       897 ACAATCCAATACCAAAGCGGGCACAATTCTCACGGAATGGATGGAGTGGAATAGATGGGGGACCT 956
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1083 ACAATCCAATACCAAAGCGGGCACAATTCTCACGGAATGGATGGAGTGGAATAGATGGGGGACCT 1142

Qy       957 CCCGCGGGCTTATACATGTCAACAGTAATGGAATTGGAGTGTTGTTATTGTTCTCCTATCTTG 1016
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1143 CCCGCGGGCTTATACAGTCAACAGTTATGGAATTGGAGTGTTGTTATTGTTCTCGTATCTTG 1202

Qy      1017 AGAGCAGAGCTAGGCCAAAAAAAGATACCTACAAACTCCTAGGAAGACTACGAATTCCCAT 1076
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1203 AGAGCAGAGCTAGGCCAAAAAAAACCTACAAACTCCTAGGAAGACTACGAATTCCCAT 1262

Qy      1077 CCAGCCCCACGGAGTCTCGGGCAAGTAGTCCTCTAAGTGCCTTGGCGGGACGGCAGT 1136
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1263 CCAGCCCCACGGAGTCTCGGGCAAGTAGTCCTCTAAGTGCCTTGGCGGGACGGCAGT 1322

Qy      1137 GGGGCGGCCGAATTTGCCTGGGGAAGGGGAAATCCGCTCTGGCCCCAACATGTGCGCCACTCCTA 1196
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1323 GGGGCGGCCGAATTTGCCTGGGGAAGGGGAAATCCGCTCTGGCCCCAACATGTGCGCCACTCCTA 1382

Qy      1197 GTTCCGGCCCCTCAGCCTCAAGTGTTTGTTATTGTCGGGTTCGGGGTTGCTTCTTCTGCCCCC 1256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1383 GCTCCGCGCCCCTCAAGTTTGTTATTGTTGGGTTCAGGGTTGCTTCTTCTGCCCC 1442
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RESULT 12
AY581858
LOCUS       AY581858      1706 bp    DNA     linear   PRI 13-NOV-2004
DEFINITION  Hylobates lar NBR1 testis isoform-like and NBR1 general
            isoform-like genes, complete sequence.
ACCESSION   AY581858
VERSION     AY581858.1  GI:51104370
KEYWORDS    .
SOURCE      Hylobates lar (common gibbon)
  ORGANISM  Hylobates lar
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hylobatidae; Hylobates.
REFERENCE   1  (bases 1 to 1706)
  AUTHORS   Jin,H., Selfe,J., Whitehouse,C., Morris,J.R., Solomon,E. and
            Roberts,R.G.
  TITLE     Structural evolution of the BRCA1 genomic region in primates
  JOURNAL   Genomics 84 (6), 1071-1082 (2004)
  PUBMED    15533724
REFERENCE   2  (bases 1 to 1706)
  AUTHORS   Roberts,R.G., Selfe,J., Jin,H., Whitehouse,C. and Solomon,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-2004) Division of Medical and Molecular Genetics,
            GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London
            SE1 9RT, UK
FEATURES             Location/Qualifiers
     source          1..1706
                     /organism="Hylobates lar"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9580"
     repeat_unit     218..565
                     /rpt_family="ARPP1"
     exon            complement(501..670)
                     /product="BRCA1"
                     /number=1
                     /pseudo
     CAAT_signal     complement(708..711)
     misc_feature    817..1301
                     /note="similar to Homo sapiens NBR1 testis isoform exon 1"
     CAAT_signal     1510..1513
     misc_feature    1545..1660
                     /note="similar to Homo sapiens NBR1 general isoform exon
                     1"
ORIGIN
Query Match           91.0%;  Score 1301.8;  DB 5;  Length 1706;
Best Local Similarity 95.5%;  Pred. No. 0;  Mismatches 57;
Matches 1374;  Conservative  0;  Mismatches 57;  Indels  8;  Gaps  3;
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Qy      1257 GCCCCATCGACGCAATCTCCACCAATCAATCAAGGGGTGGTGGTTTTTTTTGAGGGAACAACAAGTGGGTGA 1316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1443 GCCCCATCGACGCAATCTCCACCAATCAATCAAGGGGTGGTGGTTTTTTTTGAGGGAACAACAAGTGGGTGA 1502

Qy      1317 GAGCCAATCATCTTGGCGAAAAACTCGGAGAAACACAGGGGACTAGTTACTGTCTCTTTATCTTCTTTATCCGC 1376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1503 GAGCCAATCATCTTGGCGAAAAACTCGGAGAAACACAGGGGACTAGTTACTGTCTCTTTATCTTCTTTATCCGC 1562

Qy      1377 CATGTTAGATTCACCCCACAGGGATAGCGGCGCCGGCGAGAGCCGGTAGCGCGGGCGAGACGGGTCCTTG 1431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1563 CATGTTAGATTCACCCCACAGGGATAGCGGCGCCGGCGAGAGCCGGTAGCGCGGGCGAGACGGGTCCTTG 1617
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Db       302 GCCAAAAAGTTCAATATTTACACTGGCTGGCTCGCTCTTTAATAAGGGGGCATTGATTATATCCTCTG 361
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       177 TAAAGGTCACCTCATTAGTCCTTGCAGAATGAGGGCGAGAGTAGGATGCAGGCAAGCTGGGAGA 236

Db       362 TGAAGTTCACCTCATTAGTAGTGCAGAATGAGGGGCAGAGTAGAATGCAGGCAAGCTGGGAGA 421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       237 CGGAGGCCAATCATCTTGGCGGGGGCCAGTGTGTGGGGCGTGGGGAGTGGGCTGCTACTCACCG 296

Db       422 CGGAGGCCAATCGCGCGGGGGGCCAGTGTGTGGGGCGGGGGGGAGTGGGCTGCTACTCGCCG 481
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       297 GATGAAGTGAGGGTTCTCACCCCAACGCGCGGGCCCTTAGCTTCCTCCTCGGAAGGACGACACCTT 356

Db       482 GATGAAGTGAGGGATCTCACCCCAGGCGGCGGGCCCTTAGCTTCCTCGGAAGGACCGAGCACCTT 541
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       357 GGCGCGCAGCCGGAGGAAA-GGGGGTTCCACAGTTTTAATTTATCTGTAAATTCCCACACGGCTTTA 415

Db       542 GGCGCGCAGCCGGAGGAAAGGGGGTTCCACAGTTTTAATTTATCTGTAAATTCCCACACGGCTTTA 601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       416 CTGTTGCCACGGAAACCGCTGAGCAATAGCCTCTTCGAGAATAGGAAATCAAGACACAGTCA 475

Db       602 CTGTTGCCACGGAAACCGCTGAGCAATAGCCTCTTCGAGAATAGGAAATCAAGACACAGTCA 661
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       476 GAGGAAGGCGCGGGACAGAGAGAGCCTAGACATTCTCTCGCGGGGGTTTGGGCACCCAGT 535

Db       662 GAGGGAAGGCGCGGGACAGAGAGAGCCTAGACGTCTTCGGGGGTTTGGGCACCCAGT 721
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       536 CCTCCCCCTTGGTGACATAAAAGAGAAAGAGACGGGAAAAGGAGAAAGAAGAATTCTACCTGAGTTCGCC 595

Db       722 CCTCCCCCTGGTGACATAAAAGAGAAAGAGACGGGAAAAGGAGAAAGAAGAATTCTACCTGAGTTCGCC 781
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       596 GTAAAAGCGCCCGCGCCCCTCTCGCGTTCCCAGTTGCCGGCTTATTACGTCAGTAAT 655

Db       782 ATAAAAGCGCCCGCGCCCTTTTGCCTTCAGTTGCCGGCTTATTACCTCACAGTAAT 841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       656 TGCTGTACCAAAAGGTCAGAATCGCCACCCTGAAGCCTGAAATATCAGCGGTAAGCATAGAAGTAGTGTTCCA 715

Db       842 TGCTGTACAAAAGGTCAGAATCGCCACCCTGAAGCCTGAAATATCAGCGGTAAGCATAGAAGTAGTGTTCCA 901
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       716 AAGCAGTCTTAAGGAAGGAGGTCCCATTACCCACTCTTTCCGCCCTAAATGGAGGGTTCTCCAG 775

Db       902 AAGCAGTCTTAAGGAAGGAGGTCCCACTCCTCTTTCCGCCCTAAATGGAGGGTTCTCCAG 961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       776 TTTAGGTAAATAAAAGGAATTGTTGTGGGAGGTGGAGGGAAGAACTACTATTTCCAACATGC 835

Db       962 TTTAGGTAAATAAAAGGAATTGTTGTGGGGAGGTGGAGGGAAGAACTATTATTTCCAACATGC 1021
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       836 A---TTGCGGAAGGAAGAGGCCTTGGCCACACTGTTCCTTCCTTTATGGGAG 892

Db      1022 ATTGTTGCGGAACGAAAGGCCTTGGCCACACGTTCCTTGGAAAACTGTAGTCTTATGGGAG 1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       893 AGGGAACATCCAATACCAAAAGCGGCGACAAATTCTCACGTGGATAGATCGGAG 952

Db      1082 AGGAACATCCAATACCAAAAGCGGCGACAAATTCTTACGGAAAATCAGTGGATAGATTGGAG 1141
             |||||||||||||||||||||||||||||||||||||||||||||||||
Qy       953 ACCTTCCGCGGGGGCTTATACATGTCAACAGTAAATGGAGTGGTTGTTATGTTTCTTCCTAT 1012

Db      1142 ACCTTCCGCGGGGGCTTATACATGTCAACAGTTATGGAGTGGTTGTTATGTTTCTTCCTAT 1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1013 TGCTGTGAGGACGAGCTACGGCCAAAAAAAGATACCTACAAACTCCTAGGAAGGACTACGATTC 1072

Db      1202 CTTGGAGAGGCAGAGGACTAGGCCCAAGAGAAAAAGATACCTACAAACTCCTAGGAAGGACTACAATTT 1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1073 CCATCCAGCCGCCCACGAGTCTCGGCGCAAGTAGTCCCTCTAAGGTCAGTGGCCTGCGGGGACC 1132

Db      1262 CCATCCAGCCCCATGAGTCTCGGCGACAAGTAGTCTTCTAAGGTCAGTGGCCTGCGGGGACC 1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1133 CAGTGGGGGGCGGCCGGAATTTGCCTCGGGGAAGGGGAAATCCGCTCGGCCCACACTCGGCACT 1192

Db      1322 CAGTGGGGCGGCCGGAATTTGCCTCGGGGAGGGGAAAGCCGCTCGGCCCACACATCGGCGCT 1381
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1193 CCTAGTTCCGCCCCCTCAGCCTCAAATGTTTGTTTATTGTTGTGTTTTCGGGTTCAGGTGGCTTCTG 1252

Db      1382 GGTAGTTCCGCCCCCTCAGCCTCAAATGTTTGTTTATTGTTGTGTTTTCGGGTTCAGGTGGCTTCTG 1441
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Qy         1 CCGTTCCAGAACGTCTCAGCGAGCTCACGCAGCCAGTGCGCGCGCCAGTCACGTCACGTTT---TTTTCCCCCCCT 56
             ||||||||||||||||||||||||||||||||||||||||||||||||||||        ||||||||||
Db       182 CCGTTCAGAAAGTCTCAGCGAGCTCACCGCCGCCAGTCACGGCGTTTTTTTGTTTTTTTTTTTCCCC 241

Qy        57 CTACATTGCAGATGTGGGCTCCCAAATGTTGACGTTGGCCAGGACCTTTGCAAACAAGCCAG 116
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       242 CTACATTGCAGATGTGGGCTCCCAAATGTCGACGTTGGCCAGGACCTTTGCAAACAAGCCAG 301

Qy       117 GCCAAAAAGTTCAATATTTACACTGGCTGGCTCGCTCTTTAATAAGGGGGCATTGATTCTTATCCTCCG 176
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1382 GGTAGTTCCGCCCCCTCAGCCTCAAATGTTTGTTTATTGTTGTGTTTTCGGGTTCAGGTGGCTTCTG 1441
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RESULT 13
LOCUS       AY581860                1688 bp    DNA     linear   PRI 13-NOV-2004
DEFINITION  Papio anubis BRCA1 pseudogene, NBR1 testis isoform-like, and NBR1
            general isoform-like genes, complete sequence.
ACCESSION   AY581860
VERSION     AY581860.1  GI:51104372
KEYWORDS    .
SOURCE      Papio anubis (olive baboon)
  ORGANISM  Papio anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 1688)
  AUTHORS   Jin,H., Selfe,J., Whitehouse,C., Morris,J.R., Solomon,E. and
            Roberts,R.G.
  TITLE     Structural evolution of the BRCA1 genomic region in primates
  JOURNAL   Genomics 84 (6), 1071-1082 (2004)
  PUBMED    15533724
REFERENCE   2  (bases 1 to 1688)
  AUTHORS   Roberts,R.G., Selfe,J., Jin,H., Whitehouse,C. and Solomon,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-2004) Division of Medical and Molecular Genetics,
            GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London
            SE1 9RT, UK
FEATURES             Location/Qualifiers
     source          1..1688
                     /organism="Papio anubis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9555"
     repeat_unit     218..556
                     /rpt_family="ARPP1"
     exon            complement(494..657)
                     /product="BRCA1"
                     /number=1
                     /pseudo
     misc_feature    complement(695..698)
     CAAT_signal     804..1283
     misc_feature    1492..1495
                     /note="similar to Homo sapiens NBR1 testis isoform exon 1"
     CAAT_signal     1537..1642
     misc_feature    1492..1495
                     /note="similar to Homo sapiens NBR1 general isoform exon
                     1"
ORIGIN

Query Match   81.5%;  Score 1165.6;  DB 5;  Length 1688;
Best Local Similarity   91.2%;  Pred. No.   0;  Mismatches 114;
Matches 1306;  Conservative   0;  Mismatches 114;  Indels 12;  Gaps 6;
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Qy     1 CCGTCCAGACGTCTCAGCGAGCTCACGACGCGAGTCACGTGTTTTTTCCCCCCTCTAC 60
         ||||||||| ||||||||||||||||| | |||||||||||| ||||| ||||| ||||
Db   182 CCGTCCAGAAAGTCTCAGCGAGCTCACGCGCCGTCAGTCACGTTTTTCTC----CTAC 238

Qy    61 ATTGCAGATGTGGCTCCCAAGTTGACGTTGGCCAGGACCTTTGCAAACAAGCCAGGCCA 120
         |||||||||| |||||||| || |||||||||||||| ||||||||||||||||||||||
Db   239 ATTGCAGATGAGGGCTCCCAGTGTTGACGTTGGCCAGGGCTTTGCAAACAAGCCAGGCCA 298

Qy   121 AAAAGTTTCAATATTTACACTGGGGGCTCCTTTAATAAGGGGCAATTGATCTTATCCTCCGTGTAAA 180
         ||||||||||||||| ||||||||| ||||||||||||| |||||||||||||||||||||||||||
Db       |||||||||||||||||||||||||||||||

Db   299 AAAATGTTCAACATTTACACCGGGTCCTCTTAAATGAGGGGCATTGATCTTACTCCGTGAC 358
         |||| ||||| |||||||||| ||| ||| ||||| ||||||| ||||||||| ||| |||
Qy   181 GGTCACCTCAATAGTTCCTTGCAGAATGAGGGGCAGAGTAGAGTGGGGAGGA 240

Db   359 GGTCACCTCATCGTTCGGGGCAGAATGAAGGCAGAGAGTAGAGTCGGGAGACGTA 418
         |||||||||| |||| || ||||||||| || ||||||||||||| |||||| |||
Qy   241 GGCCATAGCGCGGGGGGCAGGTGTGGGGGCTGGGGGGCTGCCGGATG 300

Db   419 GGCCATGGCGGGGGGCAGCGAGTGTGGGGCTGGGGCCCGTCCTAGTTGCCGGAAG 478
         |||||| || ||||||||| | |||||||||||||   ||| ||||| ||||| ||
Qy   301 AAGTGAGGGGTCTCACCCCCAACGCGCCCTTAGCTTCCTCGGAAGGACGGACACCTTGGGCG 360

Db   479 AGGTGAGGGGCCTCACCCCAACACAGGGCCTTAACTTCCTCGGAAGGACCGAGACCTTGGGCG 538
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Qy  1253 CCCCGCCCATCGGAGCCAATCTCCACCAATCAAATGGGTCGTCGTTTGCGTTTTGAGGGACAAGTG 1312
         ||||| ||| ||| ||||||| ||||||||||||||||||| | || ||| ||||||||||||||||
Db  1442 CCCCCGCCCGGTCGACGCAATTCCACCAATCAAATGGGTCGGTGGTTCATTTGAGGGACAAGTG 1501

Qy  1313 GTGAGAGCCAATCATCTTGGCGAACACACTCGGAGAAACACAGGGGACTAGTTACTGTGCTTTTAT 1372
         || |||||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db  1502 GTAAGAGCCAATCATCTTGGCGAAAACTCGGAGAAACACAGGGGACTAGTTACTGTGCTTTTAT 1561

Qy  1373 CCCCGCCATTGTTAGATTCACCCCCCACAGGGGATTAGCGCGGAACGCCGGTCCTTG 1431
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Db  1562 CCCGCCATTGTTAGATTCACCCCACAGGGGATTAGCGCGGAACGACCGGTCCTTG 1620

Qy   541 CCTGGTGACATAAAAGAAAGAGGAGGAAAGGGTTCCACAGTTTTAATTTATCGTGTAAATTCCCACCAGT 600
         || |||| ||||||||||| ||||| |||||||||||||||| ||||| ||| |||||||||||||||||
Db   714 CCGGGTGACGTAAAAGAAAGAGACGGAAGAGGAAGAAGAATTCTACCTGAGTTTGCCATAAA 773

Qy   481 AGGGCGGGACAGAGAGAGCTTAGCATTCTCTCGGGGGCTCTGGGTTGCCACCCCCAGTTCCTCC 540
         ||||| |||||||||||||| ||||||||||||||||||||||||| ||||||||||||||||||
Db   654 AGGGAGGGACAGAGAAGAGCCTATCGTTCTCTCGGGCCTCTGGATTGGCCACCCAGTCTGCC 713

Qy   601 GCGGCCGCCCCTCTCGCCTTTACGGCTTCCAGTTGGGGCTTATTACGTCACAGTAATCGCTG 660
         ||| ||||||||||||| |||||||||||||||||| |||||||||||||| || |||||||
Db   774 GCGGCCGCCCCTCTCGCCTTTACGGCTTCCAGTTGGGGACTTATTACGTCACAGTAATCGCTG 833

Qy   661 TACCAAGGTCAGAATCGCCACCTGAGGGCCTGAGTGAATATCAGCGTTAAGATAGTAGTGTCAAAGCA 720
         ||||||||||||||||| ||||||| ||| || | || ||||| || || ||||||||| |||||||
Db   834 TACAAAAGATCAGAATCGGTACCCGGAGGCCTGAATATGAGGGTGAAGATAGTAGTGTCCAAAGCA 893

Qy   721 GTCTTAAGGAAGAGGTCCCATTACCCCACTCTTTCCGCCCACTCTTTTCCGGGAGGGTTCTCCAGTTTAG 780
         ||||| || ||||||||||||| ||||||||||||||||| ||| |||||||||||||||||||||||||
Db   894 GTCGGTAGGAGAAGAGGTCCCATTCCCCTACTCTTCTTCCGCCCTAAATGGGAGGGTCTCCAGTTTAG 953

Qy   781 GTTAAATAAAAGGATTTGTTGGGAGGTGGAGGGAAAGAAACTACTATTTCCAAACATGCCATTGC 840
         |||||| || || ||||||||||| ||||||||| ||||||| ||||||||||||| ||||||||
Db   954 GTAAATAAAAGGATTTGTTGGGAGGTGGAGGGAAAGAACTACTACTTCCAGCCATGCGTTGC 1013

Qy   841 GGAACGAAAAGGGCCTTTGGCCACACTGTTCCTTGGAAAACTGTAGTTCTTATGGGAGAGGAAACAT 900
         |||||||||| |||||| || |||| || |||| |||||  |||||||||| || |||||||||||||
Db   954 GTAAATAAAAGGATTTGTTGGGAGGTGGAGGGAAAGAACTACTACTTCCAGCCATGCGTTGC 1013
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Qy  1200 CCGCCCCTCAGCCTCAAATGTTTGTTTGTTTGTTTGTTTTTCGGGTTCGGGTTGCTTCGTCGTTT 1259
         || |||||| | ||||||||||| |||||||||||| ||| |||| ||||||||||||| | ||||
Db  1371 CCTCCCCTCGGGCCCCAAATGTTGTTTGTTTGTTTAGTTGTTGCTTCGGGTTGCTTCTGCCCGCC 1430
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RESULT 14
LOCUS   AR184045   1237 bp   DNA   linear   PAT 20-APR-2002
DEFINITION Sequence 48 from patent US 6342483.
ACCESSION   AR184045
VERSION   AR184045.1 GI:20228014
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1237)
  AUTHORS   Holt,J.T., Jensen,R.A., Page,D.L., Obermiller,P.S.,
            Robinson-Benion,C.L. and Thompson,M.E.
  TITLE   Method for detection and treatment of breast cancer
  JOURNAL   Patent: US 6342483-A 48 29-JAN-2002;
FEATURES   Location/Qualifiers
     source   1..1237
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match   63.5%; Score 909.4; DB 2; Length 1237;
Best Local Similarity   94.0%;
Matches 999; Conservative   0; Mismatches 36; Indels 28; Gaps   4;

Qy   1260 CCATCACGCAGCAATCTCCACCAATCAATGGGTGTGGTCGTTTTGAGGGACAGAAGTGGTGGAGAG 1319
          |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1431 CCGTCGACAGAATCTCCACCAATCAATGGGTGTGGTCGTTTTGAGGGACAGAAGCCGGTAAGAG 1490

Qy   1320 CCAATCATCTTGGGCGAACACACTCCGGAGAGAAACAGGGGACTAGTTACTTACTTGTCTTTATCCGGCCAT 1379
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||||||||
Db   1491 CCAATCATCTTGGGCGAAAAACTCGGCGAAAACAGGGGACTAGTTACTGTGTCTTTATCCGGCCAT 1550

Qy   1380 GTTAGATTCACCCCACAGGGATAGGGCGAGGAGCCCGGTAGGCGGACGGTCCTTG 1431
          |||||||||||||||||||||||| ||||||||||||||||||
Db   1551 GTTAGATTCACCCCACAGGGGATAGGGCGCAGGAGTTGGCGAGCGGACTGTCCTTG 1602

RESULT 15
LOCUS   AY581855   1339 bp   DNA   linear   PRI 13-NOV-2004
DEFINITION Pan troglodytes BRCA1-like and NBR2-like genes, complete sequence.
ACCESSION   AY581855
VERSION   AY581855.1 GI:51104367
KEYWORDS   .
SOURCE   Pan troglodytes (chimpanzee)
  ORGANISM Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1 (bases 1 to 1339)
  AUTHORS   Jin,H., Selfe,J., Whitehouse,C., Morris,J.R., Solomon,E. and
            Roberts,R.G.
  TITLE   Structural evolution of the BRCA1 genomic region in primates
  JOURNAL   Genomics 84 (6), 1071-1082 (2004)
  PUBMED   15533724
REFERENCE   2 (bases 1 to 1339)
  AUTHORS   Roberts,R.G., Selfe,J., Jin,H., Whitehouse,C. and Solomon,E.
  TITLE   Direct Submission
  JOURNAL   Submitted (18-MAR-2004) Division of Medical and Molecular Genetics,
            GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London
            SE1 9RT, UK
FEATURES   Location/Qualifiers
     source   1..1339
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     misc_feature   complement(110..290)
                     /note="similar to Homo sapiens BRCA1 exon 1"
     CAAT_signal   complement(374..377)
     misc_feature   440..609
                     /note="similar to Homo sapiens NBR2 exon 1"

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CAAT_signal

ORIGIN          1154..1157

Query Match     50.8%;  Score 727.6;  DB 5;  Length 1339;
Best Local Similarity   85.8%;  Pred. No. 5.2e-204;
Matches  918;  Conservative   0;  Mismatches 104;  Indels  48;  Gaps   8;

Qy     381 CACAGTTTTAATTTATCTGTAATTCCCACGGCTTTACTGTGTTGCCACCGGAA----------- 429
           ||||||||||  | ||||||||||||||| ||||||| ||||| ||||||||
Db     222 CGCAGTTTTAATTTATCTGTAATTCCCGCGCTTTTCCGGTTGCCACGGAAACCAAGGGGCT 281

Qy     430 ACCGGCTTGAGCAAATAGCCTCTCAGAATAGGAAATCAAGACACGCAGTCGAGAGGAGGCGCGGGA 489
           |||||||||||||||||||||||||||||||||||| | | ||||||||||||||||||||
Db     282 ACCGGCTAAGCAGCAGCCTCTCAGAATACGAAATCAAGGAGTACAAATCAGAGGATGGGGAGGGA 341

Qy     490 CAGAAAGAGCCTAGACATCTCTCGGGGGCTCTGGGTTGGCCACCACCAGTCCTCCCCTGG-TGA 548
           ||||||| | ||||||||||||||||||||||||||||  || ||||||||||||||| |||
Db     342 CAGAAAGAGCCAAGCTCTTCTCGGGGCCTCTGGATTGGCCACCCAGTTGTCGCCCCGGATGA 401

Qy     549 CATAAAAAAGAAAGACGGAAAAGGAAAGAAAATTCTACCTGAGTTCGCGGTAAAGCGCGCGGC 608
           |||||| | | | || |||||||||||||||||||||||| ||||| | |||||||| ||||
Db     402 CGTAAAAAGGAAAAGAACGGAAGAGGAAGAAATTCTACCTGAGTTTGCCATAAAAGTGCCTGC 461

Qy     609 CCTCTCGCGCCTCTACGGCTTCCAGTTGGCGGCTTATTACGTCACAGTAAATTGCTGTACCAAGG 668
           ||||| |||| ||| ||||||||||||||||||||||||| |||||| ||| |||||||| ||||
Db     462 CCTCTAGCCTTCAACTTTCCAGTTGCGGGCGCTTATTGCATCACAGTAATTGCTGTACCAAGG 521

Qy     669 TCAGAATCGCCACCTGAGGCCTGAATATCAGCGTAAGAATAGTGTCCAAAAGCAGTCTTAAG 728
           ||||||||||||| || | |  |||||| | |||| | ||||||||| ||||||||  ||||
Db     522 TCAGAATCGGCTACC----------------TATTGTCCAAAAGGCAGTTCGTAAG 557

Qy     729 AAGAGGTCCCATTACCCCACTCTTCCGCGCCTTAATGGATGGAGTCTTCAGTTTTAGGTAAATAA 788
           |||||||||| | | | |||||||||||||||| ||||| | ||||| ||||||| | ||||
Db     558 AAGAGGTCCCAAATCCCCACTCTTTCGCGCCTTAATGGAGTCTCCAGTTTTAGGTAAATAT 617

Qy     789 AAGGAATTGTTGGGAGGTGGGAGGGAAAG-----AACTACTATTTCCAACATCCATTCGGGA 843
           |||||| |||||||| ||||||||||||||     |||||||  | |||||||||||||||
Db     618 AAGGAATAAGGAATTGTTGGGGGGGTGGAGGGGAAATAATTATTTCCAGCATCCGTTGCGGGA 677

Qy     844 ACGAAAAGGCCTTGGCCCACACTGTTCCTTGGAAACTGATGTGTTATGGAGGAAGACATCCA 903
           |||||| |||| |||||| ||||| ||||| || |||| ||| ||| || ||||||||||||
Db     678 ATGAAAAGGTCTTCGCCCACAGTGTTCCTTAGAAACTGTAGTCTTATGGAGAGGAACATCCA 737

Qy     904 ATACCAAAGCGGGCACAATTCTCACCGGAAATCCAGTGGATAGATTGGAGACCTCCCGCGGG 963
           || |||||||||||||| |||||||||||| |||||| |||| ||||| ||| ||||||||
Db     738 ATACCAAAGCGGGCACAATTCTCACCGGAATCCAGTGGATAGATTGGAGACCTGTGCGCG 797

Qy     964 CTTTATACATGTCAAACAGTAATGGAATGGAGTGGTTGTTATGGTTCTCCTATCTTGAGAGCAG 1023
           |||||||||||| ||||| ||| || ||||| || || ||| |||||||||| ||||||||||
Db     798 CTTGTACTTGTCAACAGTTATGGACTGAAGTGTTGTTATGGTTTTTCGTATTTTTGAAAGCAG 857

Qy    1024 AGACTAGGCCAAAAAAAGATACCTACAACTC--CTAGGAAGACTACGATTCCCATCCAGCC 1082
           ||||||||||| ||||| | || |||| ||    ||||||||| ||  ||||||||||||||
Db     858 AAACTAGGCCTAAAAAAGATAACTAACTACAACTCTTTAGGGAGACTACAATTCCCATCCAGCC 917

Qy    1083 CCACGAGTCTCGGGGCAAGTAGTCCCTCTAAGTCAGTGGCCTGCGGGCACCGCAGTGGGCGC 1142
           |||| ||||| || ||||| |||||| |||||| || ||| ||||||| || || |||||||
Db     918 CCAGGAGTCTGGGGCAAGTAGTCCCTCTAAGGTCAGTGCCTGCGGGGGATGCAGTGAGCGC 977

Qy    1143 CGAATTGCCTGGGGAAGGGGAAAATCCGCTCTGGCCCACATCTGCGCCACTCCTAGTTCCG 1202
           ||||||||| ||||||||||||||||||||||||||||||| | |||||||||||||||||
Db     978 CGAATTGCCTGGGGCAGGGGAAAATCGGCTCTGGCCCACATCTGCGGCCACTCGTAGTTCCG 1037

Qy    1203 CCCCTCAGCCTCAATGTTGTTATGTGTTCGGGTTCAGGTTGCTTCTGCCCCG-CCCC 1261
           |||||||||| ||  | | | |||||  |||| ||||||| ||||| |||||  ||||
Db    1038 CCTCTCAGCCCCACGTGTTTGTTA---TTTTCGGGTTCAGCTTGCTTTGCCCCGTCTCC 1094

Qy    1262 ATCGACGCAATCTCCACCAATCAAATGGCGTCGGTCGTTTTGAGGGACAAGTGGTTGAGAGCC 1321
           |||||||||||||| |||| | | | |||||  | |||||||||||||||||||||| |||||
Db    1095 GTCGACGCAATCGCCACCAGTCAATGGGGTCGTCGTTTTGAGGGACAAAGTGGTTAAGAGCC 1154

Qy    1322 AATCATCTTGGCGAACACTCGGAGAAACAGGGGGACTAGTTACTACTGGTTCTTTATCCGGCCATGT 1381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1322 AATCATCTTGGCGAACACTCGGAGAAACAGGGGGACTAGTTACTACTGGTTCTTTATCCGGCCATGT 1381
```

Db   1155 AATCTTCTTGGCGAAAACGGCGGGAGAAAC--GGGACTAGTTACTACTGGTTCTTTATCCGGCCATGT 1212

Qy   1382 TAGATTCACCCCACAGGGATAGCCAAGAGCCAGAGCCGGGTAGCCAGAGCCGGGTCCTTG 1431
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||| |||
Db   1213 TAGATTCACCCCACAGAGATAGCCGCGCAGAGCTGGGCGCACGGGACGCGGGGTCTTTG 1262

Search completed: August 20, 2006, 07:12:06
Job time : 8459 secs

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ID   ACC69622 standard; DNA; 2941 BP.
XX
AC   ACC69622;
XX
DT   18-JUL-2003 (first entry)
XX
DE   Human tumour-specific promoter nucleotide sequence SEQ ID NO:1.
XX
KW   Human; tumour-specific promoter; tumour; cytostatic; ovarian cancer;
KW   gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200302519O-A1.
XX
PD   27-MAR-2003.
XX
PF   30-JAN-2002; 2002WO-JP000724.
XX
PR   14-SEP-2001; 2001JP-00279088.
XX
PA   (PRIM-) PRIMUNE KK.
XX
PI   Hamada K;
XX
DR   WPI; 2003-313358/30.
XX
PT   Tumour-specific promoter for producing e.g. transformant adenovirus to
PT   highly proliferate in ovarian cancer cells, applicable in gene therapy
PT   for treating ovarian cancer.
XX
PS   Claim 1; Page 34-36; 41pp; Japanese.
XX
CC   The present sequence represents a human tumour-specific promoter (I). The
CC   present invention describes the human tumour-specific promoter comprising
CC   bases from 1126-2941 or 2501-2941 in the sequence of (I) with 2941 base
CC   pairs. Also described: (1) another tumour-specific promoter hybridisable
CC   with the specified base sequence under stringent conditions and having a
CC   promoter function as such base sequence; (2) a cytotoxic tumour-specific
CC   virus with modification to the viral gene by using the tumour-specific
CC   promoter to cause specific proliferation in tumour cells or tissue; and
CC   (3) treating tumours by administration of such virus to human. (I) has
CC   cytostatic activity. The promoter can be used for producing e.g.
CC   transformant adenovirus to highly proliferate in ovarian cancer cells,
CC   which is applicable in gene therapy for treating ovarian cancer. When
CC   applied in clinical use, the produced transformant virus has reduced side
CC   -effects, and therefore larger quantities can be administered
XX
SQ   Sequence 2941 BP; 717 A; 825 C; 690 G; 709 T; 0 U; 0 Other;

Query Match             97.2%;  Score 1391;  DB 8;  Length 2941;
Best Local Similarity   100.0%;
Matches  1391;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         1 CCGTCCAGGAACGTCTCAGCGAGCTCACGACGCGCAGTCACGTTTTTTCCCCCCCTAC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1551 CCGTCCAGGAACGTCTCAGCGAGCTCACGACGCGCAGTCACGTTTTTTCCCCCCCTAC 1610

Qy        61 ATTGCAGATGTGGCTCCCAATGTTGACGTTGGCCACGACCTTGCAAACAAGCCAGGCCA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1611 ATTGCAGATGTGGCTCCCAATGTTGACGTTGGCCACGACCTTGCAAACAAGCCAGGCCA 1670

Qy       121 AAAGTTTCAATATTACACTGGCGTGCTTTATTAAATAAGGACATTGACTTATCCTCCGTAAA 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1671 AAAAGTTTCAATATTACACTGGCGTGCTTTATTAAATAAGGACATTGACTTATCCTCCGTAAA 1730

Qy       181 GGTGACCTCATCTAGTTCCTGCGAGAATGAGGCCAAGCTGGGAGACGGA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1731 GGTCACCTCATAGTTCCTGCAGAATCAGCCAGAGTAGATACGAGGACGGA 1790

Qy       241 GGCCCATAGCGCGGGGCGGGGCGAGTGTGGGGGCTGGGGGGAGAGCGGA 300
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db      1791 GGCCATAGCGCGGGGCGGGGCGAGTGTGGGGGCTGCCGGAGGCGGGTGCTACTCACCGGATG 1850

Qy       301 AAGTGAGGGGTTCCACCCCAACGGGGCCCTTAGCTTCCTCCGGAAGGACCACCTTGGCG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1851 AAGTGAGGGGTTCCACCCCAACGGGGCCCTTAGCTTCCTCCGGAAGGACCACCTTGGCG 1910

Qy       361 GCAGCCCGAGGAAAGGGGTTCCACAGTTTAATTATCTGTAATTCCCACACGCTTTACTGTT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1911 GCAGCCCGAGGAAAGGGGTTCCACAGTTTAATTATCTGTAATTCCCACACGCTTTACTGTT 1970

Qy       421 GCCACCGGAAACCGCTGAGCAATAGCCTTCAGAATAGGAAATCAAGACACAGTCAGAGGA 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1971 GCCACCGGAAACCGCTGAGCAATAGCCTTCAGAATAGGAAATCAAGACACAGTCAGAGGA 2030

Qy       481 AGGGGCGGGCAGAAGAGGCCTAGCATCTCTCGGGGGCTTCGGGGGCTTCGGCGCGGTCC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2031 AGGGGCGGGCAGAAGAGGCCTAGCATCTCTCGGGGGCTTCGGGGGCTTCGGCGCGGTCC 2090

Qy       541 CCTGGTGACATAAAAAGAAAGAGACGGAAAAGGAAGAAATTCTACCTGAGTTCGCGGTAAA 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2091 CCTGGTGACATAAAAAGAAAGAGACGGAAAAGGAAGAAATTCTACCTGAGTTCGCGGTAAA 2150

Qy       601 GCGCCGGGCCCTTCTCGCCTCTTACGCTTCCAGTTGCGGGCTTATTACGTCACAGTAATTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2151 GCGCCGGGCCCTTCTCGCCTCTTACGCTTCCAGTTGCGGGCTTATTACGTCACAGTAATTGCTG 2210

Qy       661 TACCAAGGTCAGAATCGCCACCTGAGGGCTGAATATCAGGTTAAGATAGTTGTTCCAAAGCA 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2211 TACCAAGGTCAGAATCGCCACCTGAGGGCTGAAATCAGGGTAAGATAGTTGTTCAAAGCA 2270

Qy       721 GTCTTAAGAGAAGAGGTCCCATTACCCCACTCTTTCCGCCCTAAATGGAGGGTCTCCAGTTTAG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2271 GTCTTAAGAGAAGAGGTCCCATTACCCCACTCTTTCCGCCCTAAATGGAGGGTCTCCAGTTTAG 2330

Qy       781 GTAAATAAAAGGATTGTTGGGAGGTGGAGGGAAAGAAACTACTATTTCCAAACATGCATTGC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2331 GTAAATAAAAGGATTGTTGGGAGGTGGGGGAGGGAAAGAAAGAACTACTATTTCCAAACATGCATTGC 2390

Qy       841 GGAACGAAAGGCCTTGGCCACACTGTTCCTTGGAAACGTAGTCTTATGGAGGAACAT 900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2391 GGAACGAAAGGCCTTGGCCACACTGTTCCTTGGAAACGTAGTCTTATGGAGGAACAT 2450

Qy       901 CCAATACCAAAGCGGGGCACAATTCTCACGGGAAATCCAGTGGATGAATGATTGGAGACCTCCGC 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2451 CCAATACCAAAGCGGGGCACAATTCTCACGGGAAATCCAGTGGATAGAATGGAGAGCCTCCGC 2510

Qy       961 GGGCTTATACATGTCAACGTAATGGATTGGGAGTGTTGTTATGTTCTCCTATCTTGAGAG 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2511 GGGCTTATACATGTCAACGTAATGGATTGGGAGTGTTGTTATGTTCTCCTATCTTGAGAG 2570

Qy      1021 CAGAGACTAGGCCCAAAAAAAAGTAACCTACAAACTCCTAGGAAGACTACGATTCCCATCCAG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2571 CAGAGACTAGGCCCAAAAAAAAGTAACCTACAAACTCCTAGGAAGACTACGATTCCCATCCAG 2630

Qy      1081 CCCCACGAGTCTCGGGCCAAGTAGTCCTCTAAGGTCAGTGGCCTGCGGGGACCGCAGTGGGC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2631 CCCCACGAGTCTCGGGCCAAGTAGTCCTCTAAGGTCAGTGGCCTGCGGGGACCGCAGTGGGC 2690

Qy      1141 GCCGGAATTGCCTGCTGGGGAAGGGAAATCCGTCTGGGCCCACATCTGCGCACTCCTAGTTC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2691 GCCGGAATTGCCTGCTGGGGAAGGGAAATCCGTCTGGGCCCACATCTGCGCACTCCTAGTTC 2750

Qy      1201 CGCCCCTCAGCCTCAATGTTGTTTGTTCGGGTTCAGGTTGCTTCTGCGCCCGCCCC 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2751 CGCCCCTCAGCCTCAATGTTGTTTGTTCGGGTTCAGGTTGCTTCTGCGCCCGCCCC 2810

Qy      1261 CATCGACGCAATCTCCACACAATCAATCAATGGGGTGGGGGACAAGTGGTGAGAGC 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2811 CATCGACGCAATCTCCACAATCAATGGGGTGGGGGACAAGTGGTGAGAGC 2870

Qy      1321 CAATCAATCTTGGCGAACACTCGGAGAAACAGGGGACTAGTTACTGTCTTTATCCGGCCATG 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2871 CAATCATCTTGGCGAACACTCGGAGAAACAGGGGACTAGTTACTGTCTTTATCCGGCCATG 2930
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Qy     1381 TTAGATTCACC 1391
            |||||||||||
Db     2931 TTAGATTCACC 2941
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